

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 00:33:30 ; Search time 5733.61 Seconds  
(without alignments)  
10888.092 Million cell updates/sec

Title: US-09-979-558a-1  
Perfect score: 1526  
Sequence: 1 ttgtatcatgctccagatt.....acctggcgctggaacaccc 1526

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues  
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_on.\*
- 21: em\_ov.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pi.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_hgt\_hum.\*
- 31: em\_hgt\_inv.\*
- 32: em\_hgt\_other.\*
- 33: em\_hgt\_mus.\*
- 34: em\_hgt\_pln.\*
- 35: em\_hgt\_rod.\*
- 36: em\_hgt\_mam.\*
- 37: em\_hgt\_vrt.\*
- 38: em\_sy.\*
- 39: em\_hgtgo\_hum.\*
- 40: em\_hgtgo\_mus.\*
- 41: em\_hgtgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1523	99.8	1526	1	AB016057 Psychroba
2	1523	99.8	1526	6	E58427 DNA probe f
3	1426.8	93.5	1520	1	AB016059 Psychroba
4	1426.4	93.5	1530	1	AB016058 Psychroba
5	1380.4	90.5	1536	1	AB016054 Psychroba
6	1376.2	90.2	1496	1	AY057116 Psychroba
7	1361.8	89.2	1531	1	AB016055 Psychroba
8	1359.4	89.1	1525	1	AB016056 Psychroba
9	1351.8	88.6	1403	1	AB094456 Psychroba
10	1346.2	88.2	1493	1	AF505746 Gamma pro
11	1333.8	87.4	1485	1	AY167308 Psychroba
12	1328.2	87.0	1476	1	AF505743 Bacterium
13	1327	87.0	1481	1	PGU85876 Psychrobact
14	1321.4	86.6	1494	1	PSP244766 Psychroba
15	1319.2	86.4	1491	1	PGE430828 Psychroba
16	1318.2	86.4	1492	1	PIM309942 Psychroba
17	1316	86.2	1491	1	PJ0430827 Psychroba
18	1315.6	86.2	1515	1	PGI312213 Psychroba
19	1312.8	86.0	1491	1	PGI430829 Psychroba
20	1311	85.9	1489	1	AY167286 Psychroba
21	1310.2	85.9	1449	1	AY165583 Unculture
22	1308.2	85.7	1494	1	AF441201 Psychroba
23	1308.2	85.7	1494	1	AF441202 Psychroba
24	1306.6	85.6	1502	1	MPG308373 Marine ps
25	1305.4	85.5	1462	1	PGU85877 Psychrobact
26	1302.2	85.4	1491	1	PGI430830 Psychroba
27	1302.4	85.3	1451	1	AF005192 Moraxella
28	1302	85.3	1457	1	AF468390 Arctic se
29	1301.2	85.3	1526	1	UBA440989 Antarctic
30	1300	85.2	1462	1	PGU85879 Psychrobact
31	1299.6	85.2	1469	1	AF260715 Psychroba
32	1298.4	85.1	1463	1	AY167281 Psychroba
33	1298.2	85.1	1445	1	AF468383 Arctic se
34	1298.2	85.1	1488	1	PAF297439 Psychroba
35	1297	85.0	1463	1	AY167301 Psychroba
36	1296.8	85.0	1478	1	PSU85875 Psychrobact
37	1296.4	85.0	1458	1	PGI539102 Psychroba
38	1296.2	84.9	1496	1	PPA421528 Psychroba
39	1294.6	84.8	1483	1	AF468396 Arctic se
40	1291.2	84.6	1441	1	PGU85878 Psychrobact
41	1290.4	84.6	1510	1	PSP310992 Psychroba
42	1287.2	84.4	1441	1	AY165598 Unculture
43	1286.8	84.3	1493	1	AF505725 Bacterium
44	1278	83.7	1454	1	AY167289 Psychroba
45	1274.6	83.5	1425	1	AF505739 Bacterium

ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,  
strain:NIBH P2K6(T)(=IFO 16279(T)).  
1526 bp DNA linear BCT 10-MAY-2000  
ACCESSION AB016057.1 GI:6691638  
VERSION AB016057  
KEYWORDS 16S ribosomal RNA.  
SOURCE Psychrobacter pacificensis  
ORGANISM Psychrobacter pacificensis  
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
Moraxellaceae; Psychrobacter.  
REFERENCE 1 (sites)  
AUTHORS Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.  
TITLE Phylogenetic analysis of psychrophilic bacteria isolated from the

Japan trench, including a description of the deep-sea species  
*Psychrobacter pacificensis* sp. nov  
 Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)  
 20222194  
 JOURNAL MEDLINE  
 10758895  
 PubMed  
 2 (bases 1 to 1526)  
 Maruyama, A. and Kitamura, K.  
 Direct Submission  
 Submitted (07-JUL-1998) Akihiro Maruyama, National Institute of  
 Bioscience and Human-Technology, Department of Applied and  
 Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,  
 Japan (E-mail:maruyama@nibin.go.jp, Tel.:+81-298-54-6062,  
 Fax:+81-298-54-6412)  
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Db 661 TAGAATTCAGGTGTAGCGGTGAATGCGTAGAGATCTCGAAGGAATACCGATGGCAGG 720  
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 QY 901 CAATGAATTAAGCGGCGCCGACACAGCGGTGGAGCATGTGGTTAAATTCGATCAACG 960  
 Db 901 CAATGAATTAAGCGGCGCCGACACAGCGGTGGAGCATGTGGTTAAATTCGATCAACG 960  
 QY 961 CGAAGAACCTTACCTGGTCTTGACATACAGAAATCTTTAGATACAGAGAGTCCCTTC 1020  
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## RESULT 2

E58427  
 LOCUS  
 DEFINITION  
 E58427 DNA probe for detecting novel psychrophile.  
 E58427  
 ACCESSION  
 E58427.1 GI:18622289  
 VERSION  
 E58427.1  
 KEYWORDS  
 JP 2000333680-A/1.  
 SOURCE  
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 ORGANISM  
 unclassified  
 unclassified  
 1 (bases 1 to 1526)  
 REFERENCE  
 Maruyama, A., Kitamura, K. and Kurane, R.  
 DNA probe for detecting novel psychrophile  
 PAT 31-JAN-2002

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: August 20, 2003, 00:33:30 ; Search time 5733.61 seconds  
(without alignments)  
10888.092 Million cell updates/sec

Title: US-09-979-558a-1  
Perfect score: 1526  
Sequence: 1 ttgtgatcgggtccagatt.....acctggcggtgacacctc 1526

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 2888711 seqs, 2045481386 residues  
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenBank:  
1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
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13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
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39: em.htgo\_hum.\*  
40: em.htgo\_mus.\*  
41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1523	99.8	1526	1	AB016057 Psychroba
2	1523	99.8	1526	6	E58427 DNA probe f
3	1426.8	93.5	1520	1	AB016059 Psychroba
4	1426.4	93.5	1530	1	AB016058 Psychroba
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6	1376.2	90.2	1496	1	AY057116 Psychroba
7	1361.8	89.2	1531	1	AB016055 Psychroba
8	1359.4	89.1	1525	1	AB016056 Psychroba
9	1351.8	88.6	1403	1	AB094456 Psychroba
10	1346.2	88.2	1493	1	AF505746 Gamma pro
11	1333.8	87.4	1485	1	AY167308 Psychroba
12	1328.2	87.0	1476	1	AF505743 Bacterium
13	1327	87.0	1481	1	PG085876 Psychrobact
14	1321.4	86.6	1494	1	PSP244766 Psychroba
15	1319.2	86.4	1491	1	PGE430828 Psychroba
16	1318.2	86.4	1492	1	PIK309942 Psychroba
17	1316	86.2	1491	1	PJ0430827 Psychroba
18	1315.6	86.2	1515	1	PGL312213 Psychroba
19	1312.8	86.0	1491	1	PGL430829 Psychroba
20	1311	85.9	1489	1	AY167286 Psychroba
21	1310.2	85.9	1449	1	AY165583 Unculture
22	1308.2	85.7	1494	1	AF441201 Psychroba
23	1308.2	85.7	1494	1	AF441202 Psychroba
24	1306.6	85.6	1502	1	MPS308373 Marine ps
25	1305.4	85.5	1462	1	PG085877 Psychrobact
26	1303.2	85.4	1491	1	PGL430830 Psychroba
27	1302.4	85.3	1451	1	AF005192 Moraxella
28	1302	85.3	1457	1	AF468390 Arctic se
29	1301.2	85.3	1526	1	UBA440989 Antarctic
30	1300	85.2	1462	1	PG085879 Psychrobact
31	1299.6	85.2	1469	1	AF260715 Psychroba
32	1298.4	85.1	1463	1	AY167281 Psychroba
33	1298.2	85.1	1445	1	AF468383 Arctic se
34	1298.2	85.1	1488	1	PAF297439 Psychroba
35	1297	85.0	1453	1	AY167301 Psychroba
36	1296.8	85.0	1478	1	PS085875 Psychrobact
37	1296.4	85.0	1458	1	PGL539102 Psychroba
38	1296.2	84.9	1496	1	PEA421528 Psychroba
39	1294.6	84.8	1483	1	AF468396 Arctic se
40	1291.2	84.6	1441	1	PG085878 Psychrobact
41	1290.4	84.6	1510	1	PSP310992 Psychroba
42	1287.2	84.4	1441	1	AY165598 Unculture
43	1286.8	84.3	1493	1	AF505725 Bacterium
44	1278	83.7	1454	1	AY167289 Psychroba
45	1274.6	83.5	1425	1	AF505739 Bacterium

ALIGNMENTS

RESULT 1  
LOCUS AB016057  
DEFINITION Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,  
strain: NIBH P2K6(T) (=IFO 16279(T)).  
ACCESSION AB016057.1 GI:6691638  
VERSION 16S ribosomal RNA.  
KEYWORDS Psychrobacter pacificensis  
SOURCE Psychrobacter pacificensis  
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
Moraxellaceae; Psychrobacter.  
REFERENCE 1 (sites)  
AUTHORS Maruyama, A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T.  
TITLE Phylogenetic analysis of psychrophilic bacteria isolated from the

Japan Trench, including a description of the deep-sea species  
*Psychrobacter pacificensis* sp. nov  
 Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000).  
 20222194  
 10758895  
 REFERENCE 2 (bases 1 to 1526)  
 AUTHORS Maruyama, A. and Kitamura, K.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of  
 Bioscience and Human-Technology, Department of Applied and  
 Environmental Microbiology, 1-1 Higashi, Tsukuba, Ibaraki 305-8566,  
 Japan (E-mail: maruyama@nib.ac.jp, Tel: +81-298-54-6062,  
 Fax: +81-298-54-6412)

FEATURES  
 Location/Qualifiers  
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 /product="16S ribosomal RNA"  
 BASE COUNT 401 a 332 c 467 g 323 t 3 others  
 ORIGIN

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 Matches 1526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 421 AGCAGCTTAAAGCAGTGAAGAGACTCTCGGTTAATACCCGGGACGATGACATTAGCTG 480  
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 SOURCE unidentified  
 ORGANISM unclassified  
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 AUTHORS Maruyama, A., Kitamura, K. and Kurane, R.  
 TITLE DNA probe for detecting novel psychrophile



JOURNAL Patent: JP 2000333680-A 1 05-DEC-2000;  
 AGENCY OF IND SCIENCE & TECHNOL  
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 PF 25-MAY-1999 JP 1999145342  
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 REFERENCE  
 1 (sites)  
 AUTHORS Maruyama A., Honda D., Yamamoto H., Kitamura K. and Higashihara T.  
 TITLE Phylogenetic analysis of psychrophilic bacteria isolated from the

Japan Trench, including a description of the deep-sea species  
 Psychrobacter pacificensis sp. nov  
 Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)  
 20222194  
 10758895  
 2 (bases 1 to 1520)  
 Maruyama, A. and Kitamura, K.  
 Direct Submission  
 Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of  
 Bioscience and Human-Technology, Department of Applied and  
 Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,  
 Japan [E-mail: maruyama@nibh.go.jp, Tel: +81-298-54-6062,  
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## FEATURES

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LOCUS  
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Psychrobacter pacificensis  
 strain:NIBH P2K17.

AB016058  
 VERSION

AB016058.1  
 GI:6691639

16S ribosomal RNA  
 KEYWORDS

Psychrobacter pacificensis  
 SOURCE

Psychrobacter pacificensis  
 ORGANISM

REFERENCE  
 1 (sites)

Maruyama, A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T.  
 AUTHORS

Phylogenetic analysis of psychrophilic bacteria isolated from the  
 TITLE

Japan Trench, including a description of the deep-sea species  
 Psychrobacter pacificensis sp. nov

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 Moraxellaceae; Psychrobacter.

Psychrobacter pacificensis

Psychrobacter pacificensis

Psychrobacter pacificensis

Psychrobacter pacificensis

Psychrobacter pacificensis

Psychrobacter pacificensis

Psychrobacter pacificensis

Psychrobacter pacificensis

JOURNAL Int. J. Syst. Evol. Microbiol., 50 Pt 2, 835-846 (2000)  
 MEDLINE 20222194  
 PUBMED 10758895  
 REFERENCE 2 (bases 1 to 1530)  
 AUTHORS Maruyama, A. and Kitamura, K.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of Bioscience and Human-Technology, Department of Applied and Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566, Japan (E-mail:maruyama@nibh.go.jp, Tel.:+81-298-54-6062, Fax:+81-298-54-6412)

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 REFERENCE  
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 Maruyama, A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T.  
 Phylogenetic analysis of psychrophilic bacteria isolated from the  
 Japan Trench, including a description of the deep-sea species  
 psychrobacter pacificensis sp. nov  
 Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)  
 JOURNAL 20222194  
 MEDLINE



King's College London, Guy's Hospital, London SE1 9RT, United Kingdom

REMARK Direct Submission

REFERENCE 3 (bases 1 to 1496)

AUTHORS Zandvliet,D., Coleman,D. and Coates,A.

TITLE Direct Submission

JOURNAL Submitted (25-SEP-2001) Medical Microbiology, St George's Hospital Medical School, Cranmer Terrace, London SW17 0RE, United Kingdom

FEATURES

source Location/Qualifiers

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QY 269 ACATCTGTAGCTGTGCTGAGAGGATGATCAGCACACCGGGACTGAGACACGGCCCGGA 328

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QY 329 CT-CTACGGAGGACAGCTGGGGAATATTGGACATFNGNGGAAACCCCTGATCCAGCCAT 387

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QY 388 GCCCGGTGTGTAAGAGCGCTTTTGGTTGTAAAGCACTTAAGCAGTGAAGAGACTCT 447

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QY 568 GCCTAGTGTGCTTGAATAGTCAAGTGAATCCCGGCTTAACCTGGGACACTGATCT 627

Db 550 GCCTAGTGTGCTTGAATAGTCAAGTGAATCCCGGCTTAACTGGGACACTGATCT 609

QY 628 GAACTGTAGGCTAGTGTAGAGGGAAGTAGAATTCAGGTGTAGCGGTGAATG 687

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QY 688 GCTAGAGATCTGAAGGAATACCGATGCGGAGGAGGAGGCTTCTGGCATCATACTGACACTG 747

Db 670 GCTAGAGATCTGAAGGAATACCGATGCGGAGGAGGAGGCTTCTGGCATCATACTGACACTG 729

QY 748 AGGCTGAAAGCGTGGGTAGCAACACAGGATTAGATACCTGGTAGTCCACGCCGTAAACG 807

Db 730 AGGTCGAAGCGTGGGTAGCAACACAGGATTAGATACCTGGTAGTCCACGCCGTAAACG 789

QY 808 ATGCTCTACTAGTCTGTTGGGTCCCTTGAAGACTTAGTGACGCACTAAGCAATAAGTAGA 867

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QY 928 CGGCTGGGAGTACGGCGCAAGGTTAAACTCAATGAATGACGGGGGCCGCCACAA 987

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Db 1330 CAGATGCCCGGGTGAATACGTTCCCGGCTTGTACACACCGCCCGCTCACACCAATGGGA 1389

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QY 1468 ATGACTGGGGTGAAGTCGTAACAAGTAGCCGTAGGGGAACCTGCGGC 1515

Db 1449 ATGACTGGGGTGAAGTCGTAACAAGTAGCCGTAGGGGAACCTGCGGC 1496

RESULT 7

AB016055 1531 bp DNA linear BCT 10-MAY-2000

LOCUS Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,

DEFINITION strain:NTBH P2J3.

AB016055

ACCESSION AB016055

VERSION AB016055.1 GI:6691636

KEYWORDS 16S ribosomal RNA

SOURCE Psychrobacter pacificensis

ORGANISM Psychrobacter pacificensis

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

Moraxellaceae; Psychrobacter.

REFERENCE 1 (sites)

AUTHORS Maruyama A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T.

TITLE Phylogenetic analysis of psychrophilic bacteria isolated from the Japan Trench, including a description of the deep-sea species Psychrobacter pacificensis sp. nov

JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)

MEDLINE 20222194

PUBMED 10758895





TITLE Direct Submission  
JOURNAL Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of Bioscience and Human Technology, Department of Applied and Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566, Japan (E-mail:maruyama@nibh.go.jp, Tel:+81-298-54-6062, Fax:+81-298-54-6412)

FEATURES Location/Qualifiers  
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BASE COUNT 398 a 334 c 468 g 325 t  
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Best Local Similarity 97.2%; Pred. No. 0;  
Matches 1456; Conservative 0; Mismatches 34; Indels 8; Gaps 7;

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RESULT 9  
AB094456  
LOCUS AB094456 1403 bp DNA linear BCT 16-JAN-2003  
DEFINITION Psychrobacter sp. MJVP.15.12 gene for 16S rRNA, partial sequence.  
ACCESSION AB094456  
VERSION AB094456.1 GI:27807566  
KEYWORDS  
SOURCE  
ORGANISM  
Psychrobacter sp. MJVP.15.12  
Psychrobacter sp. MJVP.15.12  
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
Moraxellaceae; Psychrobacter.  
1  
Inagaki, F., Suzuki, M., Takai, K. and Horikoshi, K.  
Microbial community structure in subseafloor sediments from the Sea  
of Okhotsk  
Published Only in Database (2003)  
REFERENCE  
2 (bases 1 to 1403)  
JOURNAL  
AUTHORS  
TITLE  
DIRECT SUBMISSION  
Inagaki, F.  
Submitted (23-OCT-2002) Fumio Inagaki, Japan Marine Science &  
Technology Center, Subground Extremophile Retrieval (SUGAR) Project,  
Frontier Research System for Extremophiles; Natsushima-cho 2-15,  
Yokosuka 237-0061, Japan (E-mail:inagaki@jamstec.go.jp,  
Tel:81-468-67-9687, Fax:81-468-67-9715)

FEATURES		Location/Qualifiers	
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Best Local Similarity 99.4%; Pred. No. 0;			
Matches 1386; Conservative 0; Mismatches 5; Indels 3; Gaps 3;			
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QY	150	GAACCTCGAATTAATACCGCATAGCT-CTACGGGAGAAAGCAGGGGNTCAATTAGACCTTG	208
Db	130	GAACCTCGAATTAATACCGCATAGCTCTACGGGAGAAAGCAGGGGATCAATTAGACCTTG	189
QY	209	CGCTATTAGATGAGCTTAAGTCGGATAGCTAGATGTTGGGGTAAAGGCTACCATCGG	268
Db	190	CGCTATTAGATGAGCTTAAGTCGGATAGCTAGATGTTGGGGTAAAGGCTACCATCGG	249
QY	269	ACGATCTGAGTGTCTGAGAGGATGATCAGCCACCGGAGTCTAGACACGGCCCGGA	328
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QY	508	CAGCAGCCGGTAAATACAGAGGTGCAAGCGTTAATCGGAATTAATGCGCGTAAAGCGA	567
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Db	670	CGTAGAGATCTGAAGGAATACCGATGCGGAGGAGCTTCTCGGCATCATCTGACACTG	729
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Db	730	AGGCTCGAAGGCTGGGTAGCAACAGATTAGATACCTGGTAGTCCAGCGCGTAAAGC	789
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1390

GTTGATTGCACAG 1403

RESULT 10

AF505746

1493 bp DNA linear BCT 31-JAN-2003

LOCUS

Gamma proteobacterium UMB21A 16S ribosomal RNA gene, partial

DEFINITION

sequence.

ACCESSION

AF505746

VERSION

AF505746.1 GI:28173023

KEYWORDS

SOURCE

gamma proteobacterium UMB21A

ORGANISM

gamma proteobacterium UMB21A

REFERENCE

1 (bases 1 to 1493)

AUTHORS

Tang,R.J. and Cooney,J.J.

TITLE

Tributyltin-resistant, biofilm-forming bacteria isolated from

JOURNAL

Boston Harbor, MA

REFERENCE

2 (bases 1 to 1493)

AUTHORS

Tang,R.J. and Cooney,J.J.

TITLE

Direct Submission

JOURNAL

Submitted (23-APR-2002) Environmental, Coastal and Ocean Sciences,

FEATURES

University of Massachusetts Boston, 100 Morrissey Blvd., Boston, MA

Source

02125-3393, USA

Location/Qualifiers

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/mol\_type="genomic DNA"

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VERSION	AY167308.1	GI:28624950			
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SOURCE	Psychrobacter glacincola				
ORGANISM	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Psychrobacter.				
REFERENCE	1 (bases 1 to 1485)				
AUTHORS	Brinkmeyer, R., Knittel, K., Juergens, J., Weyland, H., Amann, R. and Helmke, E.				
TITLE	Diversity and Structure of Bacterial Communities in Arctic versus Antarctic Sea Ice: A Comparison				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1485)				
AUTHORS	Brinkmeyer, R., Knittel, K., Juergens, J., Weyland, H., Amann, R. and Helmke, E.				
TITLE	Direct Submission				
JOURNAL	Submitted (21-OCT-2002) Alfred Wegener Institute for Polar and Marine Research, Am Handelshafen 12, Bremerhaven D-27570, Germany				
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ORIGIN					

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VERSION U85876.1 GI:1850408
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REFERENCE 1 (bases 1 to 1481)
AUTHORS Bowman, J.P., McCammon, S.A., Brown, M.V., Nichols, D.S. and
McMeekin, T.A.
TITLE Diversity and association of psychrophilic bacteria in Antarctic
sea ice
JOURNAL Appl. Environ. Microbiol. 63 (8), 3068-3078 (1997)
MEDLINE 97394931
PUBMED 9251193
REFERENCE 2 (bases 1 to 1481)
AUTHORS Bowman, J.P., McCammon, S.A., Brown, M.V. and McMeekin, T.A.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-1997) Antarctic CRC, University of Tasmania, GPO
Box 252-80, Hobart, Tasmania 7001, Australia
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AUTHORS	Fritz, I.
TITLE	Das Bakterioplankton im Westlichen Mittelmeer. Analyse der taxonomischen Struktur freilebender und partikelgebundener bakterieller Lebensgemeinschaften mit mikrobiologischen und molekularbiologischen Methoden
JOURNAL	Thesis (2000) Gemeinsame Naturwissenschaftliche Fakultät, Technische Universität Carolo-Wilhelmina Braunschweig, Braunschweig, GERMANY
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GenCore version 5.1.1.6

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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 5105512

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## SUMMARIES

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2	1211	79.4	269223	22 AAF28554	Genomic fragment #
3	1195	78.3	1485	12 AAQ13256	16S rRNA gene (par
4	1158	75.9	1335	20 AAX83569	16S rDNA gene frag
5	1153.2	75.6	1528	20 AAX83570	16S rDNA gene frag
6	1153.2	75.6	1535	20 AAX83571	16S rDNA gene frag
7	1129.2	74.0	1535	20 AAX83568	16S rDNA gene frag
8	1121.4	73.5	1529	20 AAX83564	16S rDNA gene frag

9	1121.4	73.5	1529	20 AAX83567	16S rDNA gene frag
10	1119.8	73.4	1529	20 AAX83565	16S rDNA gene frag
11	1119.8	73.4	1529	20 AAX83566	16S rDNA gene frag
12	1098.6	72.0	1501	22 AAI84997	Polyhydroxyalkanol
13	1098.6	72.0	1501	22 AAI84998	Polyhydroxyalkanol
14	1098.6	72.0	1501	22 AAH77497	Pseudomonas jessen
15	1098.6	72.0	1501	22 AAS12097	Pseudomonas jessen
16	1098.6	72.0	1501	23 AAI64177	Pseudomonas jessen
17	1098.6	72.0	1501	24 AAL39554	Pseudomonas jessen
18	1098.6	72.0	1501	24 AAI67771	Nucleotide sequenc
19	1098.6	72.0	1501	24 AAI66302	Pseudomonas jessen
20	1096.4	71.8	1566	17 AAT18643	16S ribosomal RNA
21	1095.6	71.8	1528	22 AAF76235	Cycloclasticus pug
22	1090.4	71.5	1494	25 ABX16332	Aliphatic hydrocar
23	1083.6	71.0	1480	24 AAL50855	Benzene-degrading
24	1078.8	70.7	1480	24 AAL50856	Benzene-degrading
25	1074.4	70.4	1542	17 AAT18759	E. coli 16S riboso
26	1070.8	70.2	1467	22 AAS11023	Pseudomonas aerugi
27	1070.8	70.2	5341	20 AAX24986	E. coli MG1655 rrr
28	1070.6	70.2	1540	10 AAN91514	Escherichia coli 1
29	1069.2	70.1	1542	17 AAT29140	Escherichia coli 1
30	1069.2	70.1	1542	22 AAF75410	E. coli 16S rRNA.
31	1069.2	70.1	1542	22 AAG62270	Escherichia coli r
32	1069.2	70.1	1542	24 ABN85800	Escherichia coli 1
33	1067.6	70.0	1489	24 ABS71622	Klebsiella pneumon
34	1067.6	70.0	1542	22 AAF23015	E. coli 16S rRNA s
35	1067.6	70.0	5097	20 AAX44983	E. coli MG1655 rrr
36	1066.8	69.9	1529	22 AAF76236	Cycloclasticus pug
37	1066	69.9	5105	20 AAX24989	E. coli MG1655 rrr
38	1064.4	69.8	5098	20 AAX24984	E. coli MG1655 rrr
39	1062.8	69.6	5014	20 AAX24987	E. coli MG1655 rrr
40	1062.6	69.6	1541	22 AAS11022	Salmonella typhimu
41	1061.6	69.6	1526	22 AAF76237	Cycloclasticus pug
42	1060.2	69.5	1506	24 ABS71613	Escherichia coli 1
43	1059.6	69.4	1542	14 AAQ45119	E. coli 16S rRNA f
44	1058.8	69.4	5013	20 AAX24985	E. coli MG1655 rrr
45	1058.2	69.3	1549	21 AAA65897	E. coli proliferat

## ALIGNMENTS

RESULT 1	
AAC87531	
ID AAC87531 standard; DNA; 1526 BP.	
XX AC AAC87531;	
XX AC	
XX DT 13-MAR-2001 (first entry)	
XX DE Psychrobacter pacificensis NIBH P2K6 16S rDNA, SEQ ID NO:1.	
XX XX	
KW 16S rDNA; species-specific detection; identification;	
KW psychrophilic bacterium; oceanic circulation; Psychrobacter;	
KW strain NIBH P2K6; ds.	
XX OS Psychrobacter pacificensis.	
XX PN WO200071705-A1.	
XX PD 30-NOV-2000.	
XX PF 25-MAY-2000; 2000WO-JP03372.	
XX PR 25-MAY-1999; 99JP-0145342.	
XX PR 30-MAR-2000; 2000WO-JP02045.	
XX XX (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.	
XX PI Maruyama A, Kitamura K, Kurane R;	
XX DR WPI; 2001-025158/03.	



PT DNA probe originating from psychrotrophic bacterium applicable in  
PT species-specific detection of the microorganism as indication in  
PT studying and monitoring its growth and circulation of deep-sea water  
PT with sensitivity -  
XX  
PS  
PS Claim 1; Page 30; 37pp; Japanese.  
XX  
CC The invention relates to a 1526 bp Psychrobacter pacificensis 16S rDNA  
CC sequence (AAC87531) and an oligonucleotide probe (AAC87532) comprising  
CC part of the Psychrobacter pacificensis 16S rDNA sequence which are used  
CC for monitoring the growth of psychrophilic bacteria and the circulation  
CC of deep-sea water. Psychrobacter pacificensis is an aerobic,  
CC Gram-negative, non-motile, non-spore-forming oxidase-positive bacterium  
CC originally isolated from the Japan Trench. The invention also relates to  
CC a novel method for detecting or specifically identifying Psychrobacter  
CC pacificensis, Psychrobacter glaciicola, and related species, or  
CC Psychrobacter pacificensis only via the use of the 16S rDNA sequence.  
CC The 16S rDNA sequence and derived oligonucleotide probe are useful for  
CC the species-specific detection of Psychrobacter pacificensis to study  
CC and monitor its growth as an indicator of the circulation of deep-sea  
CC water. The method of the invention is rapid, accurate and has high  
CC sensitivity and removes the need to separate and culture the biological  
CC materials. The present sequence represents the Psychrobacter  
CC pacificensis 16S rDNA.  
XX  
SQ Sequence 1526 BP; 401 A; 332 C; 467 G; 323 T; 3 other;

Query Match 99.8%; Score 1523; DB 22; Length 1526;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGATCATGGCTCCAGATTGAACGACTGGCGGCGAGCTTAACACATGCAAGTCGAGCG 60  
DB 1 TTTGATCATGGCTCCAGATTGAACGACTGGCGGCGAGCTTAACACATGCAAGTCGAGCG 60

QY 61 GAACGATGATAGCTTGTATAGGCTCGAGGCGGAGCGGTGAGTAACTACTTACGA 120  
DB 61 GAACGATGATAGCTTGTATAGGCTCGAGGCGGAGCGGTGAGTAACTACTTACGA 120

QY 121 ATCTACTAGTGGGGTAGCTCGGGAACCTCGAATTAAACCGGATAGCTTACG 180  
DB 121 ATCTACTAGTGGGGTAGCTCGGGAACCTCGAATTAAACCGGATAGCTTACG 180

QY 181 GGAAAGCAGGGGNTCATTAGACCTTGGCTATTAGATGAGCTTAAGTCGGATTAAGCTA 240  
DB 181 GGAAAGCAGGGGNTCATTAGACCTTGGCTATTAGATGAGCTTAAGTCGGATTAAGCTA 240

QY 241 GATGGTGGGTAAGAGCCCTACATGCGGACGATCTGTAGCTGGTCTGAGAGGATGATCAG 300  
DB 241 GATGGTGGGTAAGAGCCCTACATGCGGACGATCTGTAGCTGGTCTGAGAGGATGATCAG 300

QY 301 CCACCGGGAGCTGAGACACGCGCCGACTCTACGGAGGAGCAGTGGGGAATATTGA 360  
DB 301 CCACCGGGAGCTGAGACACGCGCCGACTCTACGGAGGAGCAGTGGGGAATATTGA 360

QY 361 CAATGNGGGAACCTGATCCAGCCATGCGCGGTGTGTGAAGAGGCTTTTGGTTGTA 420  
DB 361 CAATGNGGGAACCTGATCCAGCCATGCGCGGTGTGTGAAGAGGCTTTTGGTTGTA 420

QY 421 AGCAGCTTAAGCAGTGAAGAGACTCTTCGGTTAATACCGGGAGCAGTACATTAAGCTG 480  
DB 421 AGCAGCTTAAGCAGTGAAGAGACTCTTCGGTTAATACCGGGAGCAGTACATTAAGCTG 480

QY 481 CAGAAATAGCAGCGGCTAACTCTGTGCGACAGCCGCGGTAAATACAGAGGTCACAGCT 540  
DB 481 CAGAAATAGCAGCGGCTAACTCTGTGCGACAGCCGCGGTAAATACAGAGGTCACAGCT 540

QY 541 TAATCGGAATTAAGTGGCGTAAAGCGAGCGTAGTGGCTTGAATAGTCAGATGTAATC 600  
DB 541 TAATCGGAATTAAGTGGCGTAAAGCGAGCGTAGTGGCTTGAATAGTCAGATGTAATC 600

QY 601 CCGGGGCTTAAGCTGGGAACTGCATCTGAACTGTAGCTAGAGTAGGTGAGAGGAAG 660  
DB 601 CCGGGGCTTAAGCTGGGAACTGCATCTGAACTGTAGCTAGAGTAGGTGAGAGGAAG 660

DB 601 CCGGGCTTAAGCTGGGAACTGCATCTGAACTGTAGCTAGAGTAGGTGAGAGGAAG 660  
QY 661 TAGAATTTACAGTGTACGGTGAATGCGTAGAGATCTGAAGGAATACCGATGGCGAAG 720  
DB 661 TAGAATTTACAGTGTACGGTGAATGCGTAGAGATCTGAAGGAATACCGATGGCGAAG 720  
QY 721 CAGCTTCCTGGCATCATCATGACACTGAGGCTCGAAGCGTGGGTAGCAAAAGAGATTAG 780  
DB 721 CAGCTTCCTGGCATCATCATGACACTGAGGCTCGAAGCGTGGGTAGCAAAAGAGATTAG 780  
QY 781 ATACCTCTGTAGTCCACCGCTTAACGATGTCTACTAGTGTGGGTTCCTTGAAGACTT 840  
DB 781 ATACCTCTGTAGTCCACCGCTTAACGATGTCTACTAGTGTGGGTTCCTTGAAGACTT 840  
QY 841 AGTGAGGAGCTACGCAATAAGTACACCGCTGGGAGTAGCGCCGCGAGGTTAAACT 900  
DB 841 AGTGAGGAGCTACGCAATAAGTACACCGCTGGGAGTAGCGCCGCGAGGTTAAACT 900  
QY 901 CAAATGAATTGACGGGGCGCCGACAAAGCGGTGGAGCATGTGTTTAAATTCGATCAACG 960  
DB 901 CAAATGAATTGACGGGGCGCCGACAAAGCGGTGGAGCATGTGTTTAAATTCGATCAACG 960  
QY 961 CGAAGAACCTTACCTGTGTGATACATACAGAAATCTTTAGAGATACGAGAGTCCCTTC 1020  
DB 961 CGAAGAACCTTACCTGTGTGATACATACAGAAATCTTTAGAGATACGAGAGTCCCTTC 1020  
QY 1021 GGGAAATTGTGATACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
DB 1021 GGGAAATTGTGATACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
QY 1081 AAGTCCCGCAACGAGCGCAACCCCTTGTCTTAGTTACCAAGCTTCGGGTGGGAACTCTA 1140  
DB 1081 AAGTCCCGCAACGAGCGCAACCCCTTGTCTTAGTTACCAAGCTTCGGGTGGGAACTCTA 1140  
QY 1141 AGGATATCCAGTGAACAATCGAGAGAGCGGGAGCGAGCTCAAGTCAATGCGGCTT 1200  
DB 1141 AGGATATCCAGTGAACAATCGAGAGAGCGGGAGCGAGCTCAAGTCAATGCGGCTT 1200  
QY 1201 TAGCAGCAGGCTACACACCTGCTACAATGTAGTACAGAGGCGAGCTACACAGCGATG 1260  
DB 1201 TAGCAGCAGGCTACACACCTGCTACAATGTAGTACAGAGGCGAGCTACACAGCGATG 1260  
QY 1261 TGATGCAATCTCAAAAGGCTATCGTAGTCCAGATTGGAGTCTGCAACTTCGACTCCATG 1320  
DB 1261 TGATGCAATCTCAAAAGGCTATCGTAGTCCAGATTGGAGTCTGCAACTTCGACTCCATG 1320  
QY 1321 AAGTAGGAATCGCTAGTAATCGCGGATCAGAATCGCGGTGAATACGTTCCCGGGGCTT 1380  
DB 1321 AAGTAGGAATCGCTAGTAATCGCGGATCAGAATCGCGGTGAATACGTTCCCGGGGCTT 1380  
QY 1381 GTACACACCGCGCTCACACCATGGGAGTTGATTGCACCAAGAGTGTAGCTAACTTA 1440  
DB 1381 GTACACACCGCGCTCACACCATGGGAGTTGATTGCACCAAGAGTGTAGCTAACTTA 1440  
QY 1441 GTGAGGGGAGTACCCAGCGTGTGCTGATGACTGGGTTGAAGTCTGAACAGTAGCCGT 1500  
DB 1441 GTGAGGGGAGTACCCAGCGTGTGCTGATGACTGGGTTGAAGTCTGAACAGTAGCCGT 1500  
QY 1501 AGGGGAACCTGCGGCTGGATCACTC 1526  
DB 1501 AGGGGAACCTGCGGCTGGATCACTC 1526

RESULT 2  
AAF28554/c  
ID AAF28554 standard; DNA; 269223 bp.  
XX  
AC AAF28554;  
XX  
DT 04-APR-2001 (first entry)  
XX  
DE Genomic fragment #41.  
XX





Query Match	Best Local Similarity	Score	DB 12;	Length	1485;
Mismatches	Conservative	0;	Mismatches	128;	Indels
7;	Gaps	12;	Gaps	7;	
36	AGGCTTAACACATGCAAGTCGAGCGGAAACAGATGATGCTTATAGGCGTCGAGCG	95			
1	AGGCTTAACACATGCAAGTCGAGCGGAAACAGATGATGCTTATAGGCGTCGAGCG	56			
96	CCGACGCGGTCGATTAATAGGATTAACATGCTAGTACGAGCGGAAACAGCGGTCGAGCG	155			
57	CGGACGCGGTCGATTAATAGGATTAACATGCTAGTACGAGCGGAAACAGCGGTCGAGCG	116			
156	CGAATTAATACCGATACGCTTACGAGCGGAAACAGCGGTCGAGCGGTCGAGCG	215			
117	CAAGCTAATACCGATACGCTTACGAGCGGAAACAGCGGTCGAGCGGTCGAGCG	172			
216	AGATGACGCTTAAGTCGAGGATGATGCTAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGG	275			
173	AGATGACGCTTAAGTCGAGGATGATGCTAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGG	232			
276	GTAGTGTCTGAGAGGATGATGCTAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGG	334			
233	GTAGTGTCTGAGAGGATGATGCTAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGG	292			
335	GGGAGGCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGG	394			
293	GGGAGGCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGG	352			
395	GTGTGAAGAAGGCGCTTTTGGTGTGAAGAAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGG	454			

Db 1431 GGGTGAAGTCGTAACAAGTAGCCGTAGGGGAA-CTGGCGCTGGATCACCTC 1481

RESULT 4  
 AAX83569  
 ID AAX83569 standard; DNA; 1535 BP.  
 XX  
 AC AAX83569;  
 XX  
 DT 21-DEC-1999 (first entry)  
 XX  
 DE 16S rDNA gene fragment from marine bacterium, isolate K3-3.  
 XX  
 KW Monitoring; oil; contamination; sea water; detection; flagellum;  
 KW Gram-negative bacterium; Proteobacteria; glucose; carbon source;  
 KW alkane; 16S rDNA gene; ds.  
 XX  
 OS Proteobacteria.  
 XX  
 PN JP11243967-A.  
 XX  
 PD 14-SEP-1999.  
 XX  
 PF 04-MAR-1998; 98JP-0069399.  
 XX  
 PR 04-MAR-1998; 98JP-0069399.  
 XX  
 PA (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.  
 XX  
 DR WPI; 1999-564435/48.  
 XX  
 PT Monitoring of oil contamination of sea water - where oil contamination  
 PT is evaluated by detection of a microbe having properties from e.g.  
 PT having no flagellum, being a Gram-negative bacterium, belonging to  
 PT Proteobacteria, gamma subdivision, etc.2  
 XX  
 PS Claim 3; Page 7-8; 15pp; Japanese.  
 XX  
 CC The invention relates to a method for monitoring oil contamination of  
 CC sea water by detecting, in the sea water, a microbe having the following  
 CC properties: (1) it has no flagellum; (2) it is a Gram-negative bacterium;  
 CC (3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot  
 CC assimilate glucose as a single carbon source; and (5) it efficiently  
 CC assimilates at least one of 10-30C n-alkanes. This sequence represents  
 CC a fragment of the 16S rDNA gene from the microbe of the invention.  
 CC isolate K3-3.  
 XX  
 SQ Sequence 1535 BP; 375 A; 350 C; 496 G; 314 T; 0 other;

Query Match 75.9%; Score 1158; DB 20; Length 1535;  
 Best Local Similarity 87.8%; Pred. No. 0;  
 Matches 1318; Conservative 0; Mismatches 178; Indels 5; Gaps 5;

QY 30 GCGCGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATGCTTCATTAAGCGTC 89  
 DB 32 GCGCGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATGCTTCATTAAGCGTC 91  
 QY 90 GAGCNGCCGACGCGGTGAGTAATACCTAGGAATCTACCTAGTAGTGGGGATAGCTCGG 149  
 DB 92 GAGCGG-CGGACCGGTGAGTACCGGTGAGNACTGCCCATTTGTGGGGATACCTGGG 150  
 QY 150 GAACACTCGAATTAATACCCAT-ACGTTTACGGGAGAAAGCAGGGGNTCAATAGACCTTG 208  
 DB 151 GAACACTCAAGCTAATACCCATATCCCTACGGGGGAAAGCAGGGGACCTTCGGGCTTG 210  
 QY 209 CGCTATTAGATGAGCCTAAGTCGATAGCTAGTGGTGGGTAAGCCCTACCATGGCG 268  
 DB 211 TGCAGATGGATGAGCTCGCGTCGGATTAGCTAGTTGGTGGGTAAGGCCCTACCAAGGCG 270  
 QY 269 ACGATCTGATGCTGCTGAGAGGATGATCAGCCACCGGGACTGAGACACGCGCCGGA 328  
 DB 271 ACGATCGGTAGCTGGTCTGAGAGGATGATCAGCCACCGGGACTGAGACACGCGCCGGA 330

QY 329 CT-CTACGGGAGCAGCAGTGGGGAATATTGGCAATATGNGGGAACCCCTGATCCAGCCAT 387  
 DB 331 CTCCTACGGGAGCAGCAGTGGGGAATCTTGGCAATATGNGGGAACCCCTGATCCAGCCAT 390  
 QY 388 GCGCGTGTGTGAAGAAGCCCTTTTGGTTGTAAAGCACTTTTAAGCAGTGAGAACTCT 447  
 DB 391 GCGCGTGTGTGAAGAAGCCCTTAGGGTGTAAAGCACTTTTCAGCAGGAGGAGGCTTC 450  
 QY 448 TCGGTTAATACCGGGGAGGATGACATAGCTCAGAAATAGCACCCGCTACCTACTGTGTC 507  
 DB 451 GAGTTAATACCTTTGAGTACTTGAGTACTCAGAGAAGAGCACCCTAATTTCTGTGTC 510  
 QY 508 CAGCAGCCCGGTAAATACAGAGGTCGAAGCTTAATCGGAATTAATGCGGTAAAGCGA 567  
 DB 511 CAGCAGCCCGGTAAATACAGAGGTCGAAGCTTAATCGGAATTAATGCGGTAAAGCGC 570  
 QY 568 GCSTAGTGGCTTGATAAGTCAAGTGTAAATCCCGGGCTTAACCTGGGAACCTGCATCT 627  
 DB 571 GCSTAGGCGGTTTGTAAAGTCAGATGTAAAGCCCGGGCTCAACTGGGAACCTGCATTT 630  
 QY 628 GAACCTGTAGCTAGTAGTGTGAGAGGGAAGTGAATTTCAAGTGTAGCGGTGAATG 687  
 DB 631 GAAACTGGCAGGCTAGAGTGCAGTAGAGGAGGTGGAATTTCCGGTGTAGCGGTGAATG 690  
 QY 688 CGTAGAGATCTGAAGGAATACCGATGCGAAGGCAAGCTTCCTGGCATCATACTCACACTG 747  
 DB 691 CGTAGAGATCGGAAGGAACACCACTGGCGAAGCGGCTCTCTGGACTGACACTGACGCTG 750  
 QY 748 AGGCTCGAAGCGTGGGTAGCAAAACAGATTAGATACCTCGTGTAGTCCACCGCTAAAG 807  
 DB 751 AGGTGCGAAGCGTGGGAGCAAAACAGATTAGATACCTCGTGTAGTCCACCGCTAAAG 810  
 QY 808 ATGCTACTAGTGTGGTGGTCCCTT-GAGGACTTACTGACGAGCTAACGCAATAGTAG 866  
 DB 811 ATGCTACTAGTGTGGTGGTCCCTTATTTAGTATCTTGTGTGAGGATTAACGGATAGTAG 870  
 QY 867 ACCGCTGGGGAGTAGCGCCCAAGGTTAAAACTCAAAATGAATTGACGGGGCCCGCACA 926  
 DB 871 ACCGCTGGGGAGTAGCGCCCAAGGTTAAAACTCAAAATGAATTGACGGGGCCCGCACA 930  
 QY 927 AGCGGTGGACATGGGTTTAATTCGATGCAAGCGGAAGAACTTACCTGTCTTGACAT 986  
 DB 931 AGCGGTGGACATGGGTTTAATTCGATGCAAGCGGAAGAACTTACCGAGCCCTTGACAT 990  
 QY 987 ACACAGAACTCTTGTAGATACGAGTGCCTTCGGGAATTTGTGATACAGTGTGCTGATG 1046  
 DB 991 CCTCGAATCTTAGAGATAGATTGTGCTTCGGGAACGAGTGACAGGTGTGCTGATG 1050  
 QY 1047 GCTGCTCAGCTCGGTGCTGAGATGTTGGTTAAGTCCCGCAACGAGCGCAACCCCTTG 1106  
 DB 1051 GCTGCTCAGCTCGGTGCTGAGATGTTGGTTAAGTCCCGCAACGAGCGCAACCCCTTG 1110  
 QY 1107 TCCCTAGTTACCAAGCACTTCGGTGGGAACTCTTAAGGATACCTGCCAGTGACAACTGGAG 1166  
 DB 1111 TCCCTAGTTCCCAAGCACTTCGGTGGGAACTCTTAGGAGACTGCCGGTGACAAACCGGAG 1170  
 QY 1167 GAAGCGGGGACACGCTCAAGTCAATCATGCGCTTACGACCGAGGCTACACACCTGTGCTAC 1226  
 DB 1171 GAAGTGGGACGACGCTCAAGTCAATCATGCGCTTACGCGCTGGGCTACACACCTGTGCTAC 1230  
 QY 1227 AATGGTAGGTACAGAGGGGACGCTACACAGGATGTGATGGAATCTCAAAAGCTATGTC 1286  
 DB 1231 AATGGCGGTACAGAGGGGACGGAAGTCGCGAGGCCCAAGCAAAATCCCTTAAACCGCTTCG 1290  
 QY 1287 TAGTCCAGATTGAGTCTGCACTCGACTCCATCAAGTAGGTAATCGCTAGTAATTCGGGGA 1346  
 DB 1291 TAGTCCGGATTGAGTCTGCACTCGACTCCATCAAGTAGGTAATCGCTAGTAATTCGGGGA 1350  
 QY 1347 TCAGAAAGCGCGGTGAATACGTTCCCGGGCTTTGACACACGCGCCCTCACACATGGG 1406  
 DB 1351 TCAGAAAGCTGCGGTGAATACGTTCCCGGGCTTTGACACACGCGCCCTCACACATGGG 1410  
 QY 1407 AGTTGATTGCACCAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCAGGTGTGGT 1465

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Db 1411 AGTGGATTGCCACGAGTAGTGTCTTAACCTTCGGGAGACGATTACACGGTGGT 1470
QY 1466 CQATGACTGGGTGAAGTCTGAACAGGTAGCCGTAGGGGAACCTCGGGCTGGATCACT 1525
Db 1471 TCATGACTGGGTGAAGTCTGAACAGGTAGCCGTAGGGGAACCTCGGGCTGGATCACT 1530
QY 1526 C 1526
Db 1531 C 1531

RESULT 5
AAx83570
ID AAX83570 standard; DNA; 1528 BP.
XX AC
XX AAX83570;
XX 21-DEC-1999 (first entry)
XX 16S rDNA gene fragment from marine bacterium, isolate TE-9.
XX Monitoring; oil; contamination; sea water; detection; flagellum;
KW Gram-negative bacterium; Proteobacteria; glucose; carbon source;
KW alkane; 16S rDNA gene; ds.
XX
XX Proteobacteria.
XX
XX JP11243967-A.
XX
XX 14-SEP-1999.
XX 04-MAR-1998; 98JP-0069399.
XX 04-MAR-1998; 98JP-0069399.
XX (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
XX
XX WPI; 1999-564435/48.
XX
XX Monitoring of oil contamination of sea water - where oil contamination
PT is evaluated by detection of a microbe having properties from e.g.
PT having no flagellum, being a Gram-negative bacterium, belonging to
PT Proteobacteria, gamma subdivision, etc.z
XX
XX Claim 3; Page 8; 15pp; Japanese.
XX
XX The invention relates to a method for monitoring oil contamination of
CC sea water by detecting, in the sea water, a microbe having the following
CC properties: (1) it has no flagellum; (2) it is a Gram-negative bacterium;
CC (3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot
CC assimilate glucose as a single carbon source; and (5) it efficiently
CC assimilates at least one of 10-30C n-alkanes. This sequence represents
CC a fragment of the 16S rDNA gene from the microbe of the invention,
CC isolate TE-9.
XX
XX Sequence 1528 BP; 361 A; 358 C; 500 G; 309 T; 0 other;
QY
Query Match 75.6%; Score 1153.2; DB 20; Length 1528;
Best Local Similarity 87.6%; Pred. No. 0;
Matches 1315; Conservative 0; Mismatches 181; Indels 5; Gaps 5;
QY 30 GCGCGCAGGCTTAAACATCAAGTCGAGCGGAACGATGATAGCTTGTATTAGCGTTC 89
Db 25 GCGCGCAGGCTTAAACATCAAGTCGAGCGGAACGATGATAGCTTGTATTAGCGTTC 84
QY 90 GAGCNCOCGCGAGGTGAGTAACTTAGTAATCTTACCTAGTGTGGGGAGTACGTTCGGG 149
Db 85 GAGCGG-CGGACGGGTGAGTAAACACGCTGGGAATCTGCCATAGTGGGGATTAATCGGG 143
QY 150 GAACCTCGAATTAATACCGCAT-ACGCTACGGGAGAAAGCAGGGGNTCAATTAAGACTTG 208
Db 144 GAAACTCGAGCTAATACCGCATATCCCTACGCGGGGAAAGCAGGGGATCTTCGAGCTTG 203

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QY 209 CGGTATTAGATGAGCCCTAAATCGGATTAGCTAGATGGTGGGTAAAGGCTACCATGGCG 268
Db 204 CGGTATTAGATGAGCCCGCTCGGATTAGCTTGTGGTGGGTAAATGGCCACCAAGGCG 263
QY 269 AGGATCTTACTGGTCTGAGAGGATGATCAGCACACCGGACTGAGACACGCCGCCGA 328
Db 264 AGATCCCGTAACTGGTCTGAGAGGATGGCCAGTCACACCGGGACTGAGACACGCCGCCGA 323
QY 329 CT-CTACGGGAGGAGCAGTGGGGAATATTGGACAATGGGGAACCCCTGATCCAGCCAT 387
Db 324 CTCTAAGGAGGAGCAGTGGGGAATCTTGGACATGGGCGCAGCCTGATCCAGCCAT 383
QY 388 GCGCGTGTGGAAGAAGGCTTTTGGTTGTAAGACACTTAAAGCAGTGAAGAGACTCT 447
Db 384 GCGCGTGTGTAAGAAGGCTTTTGGTTGTAAGACACTTAAAGCAGTGAAGAGGAGGCTTT 443
QY 448 TCGGTTAATACCGCGGACGATGACATTAAGTGCAGATTAAGCAGCAGCGCTAACTCTGTGC 507
Db 444 GGGCTAATACCTGGAGTACTTGACCTTACCTACAGAAGAAGCACCGCTAATTTCTGTGC 503
QY 508 CAGCAGCCGCGTAAATACAGAGGGTGCAGCGTTTAAATCGGAATTAAGTGGCGCTAAAGCGA 567
Db 504 CAGCAGCCGCGTAAATACGAAGGTCGAGCGTTTAAATCGGAATTAAGTGGCGCTAAAGCGC 563
QY 568 GCGTAGTGGCTTGAATAGTCAGATGTAATCCCGGGCTTAACCTGGGGAAGTGCATCT 627
Db 564 GCGTAGGCGGTGTGTTAAGTCGGATGTGAAGCCGACGAGCTCAACCTTGAATTCATCC 623
QY 628 GAAACTGTAGGTAGATAGTGCAGAGGAGTGAAGTTCAGGTTGAGGCTGAGCGTGAATG 687
Db 624 GATAGTGGCAGCTAGAGTGCAGTGAAGGAGGTGGAATTTCCGGTGTAGCGGTGAATG 683
QY 688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGCAGCTTCTGTGCAATCATCTGACATG 747
Db 684 CGTAGAGATCGGAAGGAACACAGTGGCGAAGCGCGCTCTCTGAGCTGACACTGACGCTG 743
QY 748 AGGCTCGAAGCGTGGGTAGCAACAGAGTATAGTACCTGTGTAGTCCAGCGCGTAAAGC 807
Db 744 AGTGGCAAGCGTGGGAGCAACAGGATAGATACCTGTGTAGTCCAGCGCGTAAAGC 803
QY 808 ATGCTTACTAGTTCGTTGGGTCCCTTGAGGAC-TTASTGACGACGACGTAACGATAGTAG 866
Db 804 ATGCTTACTAGTTCGTTGGGTCCCTTAGTGACTTGGTGGCGCAGCTAACGCGATAGTAG 863
QY 867 ACCGCTGGGAGTACGGCGCGAGGTTAAACTCAATGAATTCAGCGGGGCGCGACA 926
Db 864 ACCGCTGGGAGTACGGCGCGAAGGTTAAACTCAATGAATTCAGCGGGGCGCGACA 923
QY 927 AGCGGTGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACAT 986
Db 924 AGCGGTGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTACCGGCTTGACAT 983
QY 987 ACACAGAATCTTTAGAGATACGAGAGTGCCTTCGGGAATTTGTGATACAGTGTCTGCATG 1046
Db 984 CTGCGAAGCTTTCTAGAGATAGATTGGTGCCTTCGGGAGCGCAGTGTGCTGCATG 1043
QY 1047 GCTGTGCTGACCTGCTGCTGAGATGTTGGGTTAGTCCCGCAACGAGCGCAACCCCTTG 1106
Db 1044 GCTGTGCTGACCTGCTGCTGAGATGTTGGGTTAGTCCCGCAACGAGCGCAACCCCTTG 1103
QY 1107 TCTTAGTTTACCAGCACTTCGGGTGGAACTCTAAGGATACCTGCAGTGACAAATGGAG 1166
Db 1104 TCTTAGTTTACCAGCACTTCGGGTGGAACTCTAAGGATACCTGCAGTGACAAATGGAG 1163
QY 1167 GAAGCGGGAGCAGCTCAAGTCAATCATGCGCCCTTACGACCGAGGCTTACACAGTGTCTAC 1226
Db 1164 GAAGCGGGAGCAGCTCAAGTCAATCATGCGCCCTTACGCGCTGGGCTTACACAGTGTCTAC 1223
QY 1227 AATGTTAGTACAGAGGCGAGCTACACAGGATGTGATGCGAATCTCAAAAGACCTATCG 1286
Db 1224 AATGGTTGTTAGAGAGGTTTGGGAAGTCGCGAGCGGAGCTAATCTCTCAAAAGCAATCG 1283

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QY 1167 GAAGCGGGGACGACGCTCAATCATCATATGCGCCCTTACGACACAGGCTACACAGCTGTCTAC 1226  
 DB 1171 GAAGGTGGGATGACGCTCAGGTCTCATGCGCCCTTACGCCACAGGCTACACAGCTGTCTAC 1230  
 QY 1227 AATGGTAGGTACAGAGGCGACGTACACAGCGATGTGATCGGAATCTCAAAAAGCCATATCG 1286  
 DB 1231 AATGGCGGTACAGAGGCGTCCAACTCCGAGAGTGAGCCATCCCTTAAACGCGGTG 1290  
 QY 1287 TAGTCCAGATGTGGAGTCTGCAACTCGACTCCATGAAAGTAGGAATGCTAGTAATTCGCGGA 1346  
 DB 1291 TAGTCCGATTCGAGGTCTGCAACTCGACTCCGTAAGTGGAAATGCTAGTAATTCGCGGA 1350  
 QY 1347 TCAGATGCGCGGTGATAGTTCGCGGCGCTTGTACACACGCGCGCTACACACATGGG 1406  
 DB 1351 TCAGATGTCGCGGTGATAGTTCGCGGCGCTTGTACACACGCGCGCTACACACATGGG 1410  
 QY 1407 AGTTGATTCACACAGAGTGGTTAGCCTAA-CTTACTGAGGCGGATACACACGCTGTGT 1465  
 DB 1411 AGTGGATTCACACAGAGTGGTTAGTCTAACCTTCGGAGAGAGATTAACACGCTGTGT 1470  
 QY 1466 CGATGACTGGGTGAGTCTGTAACAGGTAGCCGTAGGGGAACTGCGGCTGATGATCACT 1525  
 DB 1471 TCATGACTGGGTGAGTCTGTAACAGGTAGCCGTAGGGGAACTGCGGCTGATGATCACT 1530  
 QY 1526 C 1526  
 DB 1531 C 1531

RESULT 7  
 AAX83568  
 ID AAX83568 standard; DNA; 1535 BP.  
 XX AAX83568;  
 AC AAX83568;  
 XX 21-DEC-1999 (first entry)  
 XX 16S rDNA gene fragment from marine bacterium, isolate K2-1.  
 XX Monitoring; oil; contamination; sea water; detection; flagellum;  
 KW Gram-negative bacterium; Proteobacteria; glucose; carbon source;  
 KW alkane; 16S rDNA gene; ds.  
 XX Proteobacteria.  
 OS JP11243967-A.  
 XX 14-SEP-1999.  
 PD 04-MAR-1998; 98JP-0069399.  
 XX 04-MAR-1998; 98JP-0069399.  
 XX (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.  
 XX WPI; 1999-564435/48.  
 XX Monitoring of oil contamination of sea water - where oil contamination  
 PT is evaluated by detection of a microbe having properties from e.g.  
 PT having no flagellum, being a Gram-negative bacterium, belonging to  
 PT Proteobacteria, gamma subdivision, etc.2  
 XX Claim 3; Page 7; 15pp; Japanese.  
 XX The invention relates to a method for monitoring oil contamination of  
 CC sea water by detecting, in the sea water, a microbe having the following  
 CC properties: (1) it has no flagellum; (2) it is a Gram-negative bacterium;  
 CC (3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot  
 CC assimilate glucose as a single carbon source; and (5) it efficiently  
 CC assimilates at least one of 10-30C n-alkanes. This sequence represents  
 CC a fragment of the 16S rDNA gene from the microbe of the invention,  
 CC isolate K2-1.

XX SQ Sequence 1535 BP; 376 A; 349 C; 494 G; 316 T; 0 other;  
 Query Match 74.0%; Score 1129.2; DB 20; Length 1535;  
 Best Local Similarity 86.6%; Pred. No. 0;  
 Matches 1300; Conservative 0; Mismatches 196; Indels 5; Gaps 5;  
 QY 30 GGGGCGAGGCTTAACATATGCAATGCAAGTCGAGGGAAGATGATAGTGTGCTTATAGCGTC 89  
 DB 32 GGGGCGAGGCTTAACATATGCAATGCAAGTCGAGGGAAGATGATAGTGTGCTTATAGCGTC 91  
 QY 90 GAGNCGCGGCGGTGAGTAACTTASGAANTCTACTAGTACTAGTGGGATAGCTCTCGG 149  
 DB 92 GAGCGG-CGGAGCGGTGAGTAACTTASGAANTCTACTAGTACTAGTGGGATAGCTCTCGG 150  
 QY 150 GAAACTCGAATTAATACCGCAT-ACGTCCTACGGGAGAAAGCAGAGGGGNTCAATTAGACTTG 208  
 DB 151 GAAACTCAAGCTTAATACCGCATTAATCCCTACGGGGAAGCAGAGGGACCTTCGGGCTTG 210  
 QY 209 CGCTATTAGATGAGCTTAAGTCGGATTAAGTCGGATTAAGTCGGATTAAGTCGGATTAAG 268  
 DB 211 TGCAGATGATGAGCTTCGCGTTCGATTAAGTCGGATTAAGTCGGATTAAGTCGGATTAAG 270  
 QY 289 ACATCTGTAGTGTCTGTAGAGGATGATCAGCCACACCGGAGCTGAGACACGCGCCGGA 328  
 DB 271 ACGATCGTAGTGTCTGTAGAGGATGATCAGCCACACCGGAGCTGAGACACGCGCCGGA 330  
 QY 329 CT-CTAGGGAGGACGAGTGGGGAATTAATGGAATATGNGNGGGAACCTGATCCAGCCAT 387  
 DB 331 CTCCTACGGAGGACGAGTGGGGAATCTTGGACAATGGGGGAACCTGATCCAGCCAT 390  
 QY 388 GCAGCTGTGTGAAGAGGCTTTTGGCTGTAAAGCACTTTAAGCACTTTAAGCACTTTAAGCACT 447  
 DB 391 GCAGCTGTGTGAAGAGGCTTTTGGCTGTAAAGCACTTTAAGCACTTTAAGCACTTTAAGCACT 450  
 QY 448 TCGGTTAATACCGGCGGACGATGACATTAGCTCAGAAATAGCACCGGCTAACTCTGTGC 507  
 DB 451 GGGTTAATACCTTGGAGTACTTGAGTTACCTACAGAAGACACCGGCTAACTCTGTGC 510  
 QY 508 CAGCAGCCGCGTAAATACAGAGGCTGCAAGCGTTAATCGGAATTAATCGGAATTAATCGGA 567  
 DB 511 CAGCAGCCGCGTAAATACAGAGGCTGCAAGCGTTAATCGGAATTAATCGGAATTAATCGGA 570  
 QY 568 CGCTAGTGTGTGATTAAGTCAGATGTGAATCCCGGGCTTAACTCGGGAATGATCT 627  
 DB 571 CGCTAGGCGGTGTGATTAAGTCAGATGTGAATCCCGGGCTTAACTCGGGAATGATCT 630  
 QY 628 GAAACTTTAGCTAGATAGTGTGAGAGGAACTAGAAATTCAGGTGTAGCGGTGAAATG 687  
 DB 631 GAAACTGGCAAGCTAGAAATGCAATGAGGAGGTGGAATTTCCGGTGTAGCGGTGAAATG 690  
 QY 688 CGTAGATCTGAGGAATACCGATGCGGAGGACGCTTCCTGGCATATACATGACACTG 747  
 DB 691 CGTAGATCGGAAGGAGACACCGAGTGGGAGGCGGCTTCCTGGCATATACATGACACTG 750  
 QY 748 AGGCTCGAAAGCGTGGTAGCAAAACAGGATTAAGTACCCTGGTAGTCCACGCCCTAAAG 807  
 DB 751 AGGTGCGAAGCGTGGGAGCAACAGGATTAAGTACCCTGGTAGTCCACGCCCTAAAG 810  
 QY 808 ATGTCTACTAGTGTGGTCCCTT-GAGGACTTACTGACGAGCTACGCAATAGTAG 866  
 DB 811 ATGTCTACTAGTGTGGGAACTTACTTCTTGTGTGACGAAGTTAACGCGATAGTAG 870  
 QY 867 ACCGCTGGGAGTACGGCGCAGGTTAACTCAAAATGAATTCAGCGGGGCCCCGACA 926  
 DB 871 ACCGCTGGGAGTACGGCGCAGGTTAACTCAAAATGAATTCAGCGGGGCCCCGACA 930  
 QY 927 AGCGGTGGAGCTGGTGTAAATTCGATGCAACGCAAGAACCTTACTGCTGTGACAT 986  
 DB 931 AGCGGTGGAGCTGGTGTAAATTCGATGCAACGCAAGAACCTTACTGCTGTGACAT 990  
 QY 987 ACACAGAACTTGTGATAGATACGAGAGTGCCTTCGCGGAATTTGTGATACAGTGTCTCATG 1046  
 DB 1046 ACACAGAACTTGTGATAGATACGAGAGTGCCTTCGCGGAATTTGTGATACAGTGTCTCATG 1046

Db 991 CCTTGGAACTTTCTAGAGATGATGGTGCTTCGGGAGCCAAAGTCAGAGGTGCTGCATG 1050  
QY 1047 GCTGCTCAGTCGTCGTGAGATGTTGGTTAAAGTCCGCAACAGACGCCACCCCTTG 1106  
Db 1051 GCTGCTCAGTCGTCGTGAGATGTTGGTTAAAGTCCGCAACAGACGCCACCCCTTG 1110  
QY 1107 TCCTTACTTACCAAGCACTTCGGTGGGAACTCTAAGGATACCTCCAGTGCACAACTGGAG 1166  
Db 1111 TCCTTACTTACCAAGCACTTCGGTGGGAACTCTAAGGATACCTCCAGTGCACAACTGGAG 1170  
QY 1167 GAAGCGGGGACAGCTCAAGTCATCATGCGCCCTTACGACCAAGGCTACACAGCTGCTAC 1226  
Db 1171 GAAGGTGGGACAGCTCAAGTCATCATGCGCCCTTACGACCAAGGCTACACAGCTGCTAC 1230  
QY 1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATCGGAATCTCAAAAGCCTATCG 1286  
Db 1231 AATGGCGGTACAGAGGGCAGCGAAGTCGCGAGGCCAGCAAAATCCCTTAAACCGCTTCG 1290  
QY 1287 TAGTCCAGATTGGAGTCTGCACTCGACTCCATGAGTAGGATCGCTAGTAATCGCGGA 1346  
Db 1291 TAGTCCGGAATGGAGTCTGCACTCGACTCCATGAGTAGGATCGCTAGTAATCGCGGA 1350  
QY 1347 TCAGAATGCCGCGGTGAATACCTTCGCGGCTTGTACACACGCGCGCTCAACCATGGG 1406  
Db 1351 TCAGAATGCCGCGGTGAATACCTTCGCGGCTTGTACACACGCGCGCTCAACCATGGG 1410  
QY 1407 AGTTGATGACACAGAGTGGTGTACCTTAA-CTTAGTGAAGGCGATCAACCGGTGTGGT 1465  
Db 1411 AGTGGATTGCACAGAAAGTGGTGTAGTCTTAACCTTCGGGAGGACGATCACCACGCTGGT 1470  
QY 1466 CGATGACTGGGTGAAGTCTGTAACAGTAGTACCGGTAGGCGGCTGGGTGATCACT 1525  
Db 1471 TCATGACTGGGTGAAGTCTGTAACAGTAGTACCGGTAGGCGGCTGGGTGATCACT 1530  
QY 1526 C 1526  
Db 1531 C 1531  
RESULT 8  
AAx83564  
ID AAx83564 standard; DNA; 1529 BP.  
XX AAx83564;  
AC AAx83564;  
XX 21-DEC-1999 (first entry)  
DT 21-DEC-1999 (first entry)  
XX 16S rDNA gene fragment from marine bacterium, isolate ST-1.  
DE DE  
XX Monitoring; oil; contamination; sea water; detection; flagellum;  
KW Gram-negative bacterium; Proteobacteria; glucose; carbon source;  
KW alkane; 16S rDNA gene; ds.  
XX Proteobacteria.  
OS  
XX JP11243967-A.  
PN  
XX 14-SEP-1999.  
PD  
XX 04-MAR-1998; 98JP-0069399.  
PF  
XX 04-MAR-1998; 98JP-0069399.  
PR  
XX (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.  
PA  
XX WPI; 1999-564435/48.  
DR  
XX Monitoring of oil contamination of sea water - where oil contamination  
PT is evaluated by detection of a microbe having properties from e.g.  
PT having no flagellum, being a Gram-negative bacterium, belonging to  
PT Proteobacteria, gamma subdivision, etc.2  
XX  
PS Clam 3; Page 5; 15pp; Japanese.

XX The invention relates to a method for monitoring oil contamination of  
CC sea water by detecting, in the sea water, a microbe having the following  
CC properties: (1) it has no flagellum; (2) it is a Gram-negative bacterium;  
CC (3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot  
CC assimilate glucose as a single carbon source; and (5) it efficiently  
CC assimilates at least one of 10-30C n-alkanes. This sequence represents  
CC a fragment of the 16S rDNA gene from the microbe of the invention,  
CC isolate ST-1.  
XX  
SQ Sequence 1529 BP; 379 A; 351 C; 487 G; 312 T; 0 other;  
Query Match 73.5%; Score 1121.4; DB 20; Length 1529;  
Best Local Similarity 86.7%; Pred. No. 0;  
Matches 1302; Conservative 0; Mismatches 194; Indels 6; Gaps 6;  
QY 30 GCGCGAGGCTTAACATGCAAGTCGAGCGGAACGATGATAGCTTGTCTATTAGGGGTC 89  
Db 25 GCGCGAGGCTTAACATGCAAGTCGAGCGGAACGATGATAGCTTGTCTATTAGGGGTC 84  
QY 90 GAGNGCGGAGCGGTGAGTAACTTAGGAATCTACTAGTAGTGGGGATAGCTGGG 149  
Db 85 GAGCGG-CGAGCGGTGAGTAACTTAGGAATCTACTAGTAGTGGGGATAGCTGGG 143  
QY 150 GAACTCGAATTAATACCCCAT-ACGTTACGGGAGAAACAGAGGGGNTCATTAGACCTTG 208  
Db 144 GAAACCCAGGCTTAATACCCCATATCCCTACGGGGAAAGCAGGGGATCTCGGACCTTG 203  
QY 209 CCGTATTAGTAGGCTTAAGTCGGATTAGCTAGTGGGTAAAGGCTTACCATTGGC 268  
Db 204 TCTGATGATGAGTCGCGGTGCGGATAGCTTGTGGTAGGTAATGGCTACCAAGCGC 263  
QY 269 AGATCTGTAGCTGTGTGAGAGGATGATCAGCACACCGGACTGAGACACGCGCCGGA 328  
Db 264 ACGATCCGTAGCTGTGTGAGAGGATGATCAGCACACCGGACTGAGACACGCGCCGGA 323  
QY 329 CT-CTACGGGAGCGAGCTGGGGATATTGGCAATGNGGGAACCTTGATCCAGCAT 387  
Db 324 CTCCTACGGGAGCGAGCTGGGGATATTGGCAATGNGGGAACCTTGATCCAGCAT 383  
QY 388 GCGCGTGTGTGAAGAGCGCTTTGGTTGTAAAGCACTTTTAAGCAGTGAAGCACTCT 447  
Db 384 GCGCGGTGTGAAGAGCGCTTCGGTTGTAAAGCACTTTTAAGCAGTGAAGCACTCT 443  
QY 448 TCGGTTAATACCGCGGAGCATGACATAGCTAGTCAGAAATAGCACCGGCTAATCTGTGC 507  
Db 444 TCGGTTAATACCGGAGTACTTACGTTTACCTAGAGAAAGCAACCGGCTAATCTGTGC 503  
QY 508 CAGCAGCGCGCTAATACAGAGGTGCGAGCGTTAATCGGAATTAAGTGGCGCTAAGCGA 567  
Db 504 CAGCAGCGCGCTAATACAGAGGTGCGAGCGTTAATCGGAATTAAGTGGCGCTAAGCGC 563  
QY 568 CGTAGGTGGCTTGAATAGTCAGATGTGAAATCCCGGGCTTAACCTGGGAATCTCATCT 627  
Db 564 CGTAGGTGGCTTGAATAGTCAGATGTGAAATCCCGGGCTTAACCTGGGAATCTCATCT 623  
QY 628 GAACTGTTAGCTAGTAGTAGTGAGAGGAGTAGAATTTCAAGTGTAGCGGTGAATG 687  
Db 624 GAACTGTTAGCTAGTAGTAGTGAGAGGAGTAGAATTTCAAGTGTAGCGGTGAATG 683  
QY 688 CGTAGAGATCTGAAGGAATACCGATGAGGAGGAGCTTCTCGCATCATCTGACACTG 747  
Db 684 CGTAGAGATCTGAAGGAATACCGATGAGGAGGAGCTTCTCGCATCATCTGACACTG 743  
QY 748 AGGCTCGAAAGCGTGGGTAGCAAAACAGGATTAGTATCCCTGGTAGTCCACCGCTAAGC 807  
Db 744 AGGCTCGAAAGCGTGGGTAGCAAAACAGGATTAGTATCCCTGGTAGTCCACCGCTAAGC 803  
QY 808 ATGCTACTAGTCTGTGGGTCCCTT-GAGGACTTAGTAGCAGCAGCTAACGCAATAGTAG 866  
Db 804 ATGCTACTAGTCTGTGGGTCCCTT-GAGGACTTAGTAGCAGCAGCTAACGCAATAGTAG 863  
QY 867 ACCGCTGGGAGTAGTACGCGCGCAAGGTTAAACATCAATGAATTGACGGGGCCCGCACA 926









XX	16S rDNA gene fragment from marine bacterium, isolate Wf-2.
DE	
XX	Monitoring; oil; contamination; sea water; detection; flagellum;
KW	Gram-negative bacterium; Proteobacteria; glucose; carbon source;
KW	alkane; 16S rDNA gene; ds.
XX	
OS	Proteobacteria.
XX	
PN	JP11243967-A.
XX	
PD	14-SEP-1999.
XX	
PF	04-MAR-1998; 98JP-0069399.
XX	
PR	04-MAR-1998; 98JP-0069399.
XX	
PA	(KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
XX	
WI	WIPI; 1999-564435/48.
XX	
PT	Monitoring of oil contamination of sea water - where oil contamination
PT	is evaluated by detection of a microbe having properties from e.g.
PT	having no flagellum, being a Gram-negative bacterium, belonging to
PT	Proteobacteria, gamma subdivision, etc.z
PS	
XX	Claim 3; Page 6; 15pp; Japanese.
XX	
CC	The invention relates to a method for monitoring oil contamination of
CC	sea water by detecting, in the sea water, a microbe having the following
CC	properties: (1) it has no flagellum; (2) it is a Gram-negative bacterium;
CC	(3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot
CC	assimilate glucose as a single carbon source; and (5) it efficiently
CC	assimilates at least one of 10-30C n-alkanes. This sequence represents
CC	a fragment of the 16S rDNA gene from the microbe of the invention,
CC	isolate Wf-2.
XX	
XX	Sequence 1529 BP; 376 A; 352 C; 489 G; 312 T; 0 other;
XX	

Query Match	73.4%	Score 1119.8	DB 20	Length 1529
Best Local Similarity	86.6%	Prod. No. 0		
Matches 1301	Conservative 0	Mismatches 195	Indels 6	Gaps 6
QY	30	GGCGGAGGCTTAAACACATGCAAGTGCAGCGGAACGATGATGCTTGCTATTAGGCGTC	89	
Db	25	GGCGGAGGCTTAAACATGCAAGTGCAGCGGAACGATGCTTGCTAGGAGGCGTC	84	
QY	90	GAGNGCCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGTCGGG	141	
Db	85	GAGCGG-CGGACGGGTGAGTAACACGCTGGAATCTGCCATTAGTGGGGGATAAAGCTGGG	143	
QY	150	GAACATCGAATTAATACCGCAT-ACGCTCTACGGGAGAAAGCAGGGGTCATTAGACCTTG	208	
Db	144	GAACCCGAGCTTAATACCGCATATCCCTACGGGGGAAGCAGGGGACCTTCGGGGCCCTG	203	
QY	209	CGCTATTAGATGAGCTAAAGTCGAGATTAGCTAGATGGTGGGGTAAAGGCTACCAATGGCG	268	
Db	204	TGCTGATGATGAGCTCGCGTGGGATTAGCTTGTGGTGAGTAATGGCTACCAAGCGG	263	
QY	269	ACGATCTAGTGTCTGTGAGAGATGATACGCCACACCGGGAATGAGACACGGGCCCGGA	328	
Db	264	ACGATCCGTAGTGTCTTGTAGGAGATGATCAGCCACACCGGGAATGAGACACGGGCCCGGA	323	
QY	329	CT-CTACGGGAGCAGAGTGGGGAATATTGGACATATGNGGGAACCCGTGATCAGCAAT	387	
Db	324	CTCCTACGGGAGCAGCAGTGGGGAATCTTGGACATATGNGGGAACCCGTGATCAGCAAT	383	
QY	388	GGCGCGTGTGTGAAGAAGGCGCTTTGGTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT	447	
Db	384	GGCGCGTGTGTGAAGAAGGCGCTTCGGGTGTAAAGCACTTTCAGTAGGAGGAGAGGCTTA	443	
QY	448	TCGTTTAATACCCGGGACGATGACATTAAGTCTCAGAATAAGCACCGGCTAACTCTGTGC	507	

Db 444 TCCTTATACGATGAGTACTTGACGTACCTACAGAGACGCCGCTAATTTTCGTGC 503  
QY 508 CACACGCCCGGTAAATACAGAGGTGCAAGCGTTAATCGGAATTACTGGCGTAAAGCGA 567  
Db 504 CACACGCCCGGTAAATACAGAGGTGCGAGCGTTAATCGGAATTACTGGCGTAAAGCGC 563  
QY 568 GCGTAGGTGGCTGTAGTACAGATGTGAATCCCGCGGCTTACCTGGGAATCGATCT 627  
Db 564 GCGTAGGTGGCTGTAGTACAGATGTGAATCCCGCGGCTTACCTGGGAATCGATCT 623  
QY 628 GAAACCTGTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 687  
Db 624 GAACTGGCAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 683  
QY 688 CTTAGAGATCTGAAGATACCGATGCGGAGAGCTTCTCGGATCATCTAGCTAGCTAGCT 747  
Db 684 CTTAGAGATCTGAAGATACCGATGCGGAGAGCTTCTCGGATCATCTAGCTAGCTAGCT 743  
QY 748 AGGCTGAAAGCGTGGGTAGTCAACAGATTTAGATACCTGTAGTCCACGCCGTAAGC 807  
Db 744 AGTGGCAAGCGTGGGAGAGCAACAGATTTAGATACCTGTAGTCCACGCCGTAAGC 803  
QY 808 ATCTCTACTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 866  
Db 804 ATCTCTACTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 863  
QY 867 ACCGCTGGGAGTACGGCCGCAAGGTAACTCAATGAATGACGGGGGCCGCA 926  
Db 864 ACCGCTGGGAGTACGGCCGCAAGGTAACTCAATGAATGACGGGGGCCGCA 923  
QY 927 AGCGGTGGAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 986  
Db 924 AGCGGTGGAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 983  
QY 987 ACACAGAACTTTGTAGATACGAGAGTGCCTTCGGAATTTGTATACAGTGTCTGATG 1046  
Db 984 CTTTGAACCTTTCTAGATAGATTGTGCTTCGGAGCCCAAGTGCAGAGTGTCTGATG 1043  
QY 1047 GCTGTGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 1106  
Db 1044 GCTGTGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 1103  
QY 1107 TCCTTAGTACACGAC--TTCCGGTGGAACTCTAGGATACCTGCTAGTACAACTGGA 1165  
Db 1104 TCCTTAGTACACGACATATGTGTGGAACTCTAGGAGACTGCCGTGACAACTGGA 1163  
QY 1166 GGAAGCGGGGACGACGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 1225  
Db 1164 GGAAGTGGGGGACGACGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 1223  
QY 1226 CAATGTAGGTACAGAGGACGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 1285  
Db 1224 CAATGTAGGTACAGAGGACGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 1283  
QY 1286 GTAGTCCAGATTGGAGTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1345  
Db 1284 GTAGTCCGATGGAGTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1343  
QY 1346 ATCAGAACTCCCGGTGAATACGTTCCCGGGCCCTTGTACACACGCCCGCTCACACATGG 1405  
Db 1344 ATCAGAACTCCCGGTGAATACGTTCCCGGGCCCTTGTACACACGCCCGCTCACACATGG 1403  
QY 1406 GAGTGTAGTGCACAGAGTGGTTAGCTTAA--CTTGTAGTGGGCGCATCACCGGTGGG 1464  
Db 1404 GAGTGTAGTGCACAGAGTGGTTAGCTTAACTCTCGGAGAGAGTTCACACCGGTGGG 1463  
QY 1465 TCGATGACTGGGTGAATCTGCTTAAAGGTAGCCGTAGGGGAACTCGCGGTGGATCAC 1524  
Db 1464 TCGATGACTGGGTGAATCTGCTTAAAGGTAGCCGTAGGGGAACTCGCGGTGGATCAC 1523  
QY 1525 TC 1526  
Db 1524 TC 1525

RESULT 12  
AAI64997  
ID AAI64997 standard; DNA; 1501 BP.  
XX AAI64997;  
XX 11-DEC-2001 (first entry)  
XX Polyhydroxyalkanoic acid related Pseudomonas jessenii coding sequence.  
XX Polyhydroxyalkanoic acid; PHA; functional polymer; ds.  
OS Pseudomonas jessenii.  
XX JP2001178486-A.  
XX 03-JUL-2001.  
XX 27-DEC-1999; 99JP-0371870.  
XX 27-DEC-1999; 99JP-0371870.  
XX (CANO ) CANON KK.  
XX WPI; 2001-592590/67.  
XX Production of a polyhydroxyalkanoate useful as a functional polymer -  
XX Disclosure; Page 7-8; 10pp; Japanese.  
XX The present invention relates to a method for the production of  
XX polyhydroxyalkanoic acid (PHA). This can be used as a functional polymer.  
XX The present sequence is a Pseudomonas jessenii coding sequence which was  
XX described in the exemplification of the invention.  
XX Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;

Query Match 72.0%; Score 1098.6; DB 22; Length 1501;  
Best Local Similarity 85.9%; Pred. No. 0;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;  
QY 30 GCGCGCAGCTTAACACATGCAAGTCGCGGGAAGATGATAGCTGCTATTAGGCGTC 89  
Db 9 GCGCGCAGCTTAACACATGCAAGTCGCGGGAAGATGATAGCTGCTATTAGGCGTC 66  
QY 90 GAGCNGCCGCGAGCGGTGAGTAACTTACCTAGGAACTCTACCTAGTAGTGGGGATAGCTCGG 149  
Db 67 G---CGCGCGAGCGGTGAGTAACTTACCTAGGAACTCTACCTAGTAGTGGGGATAGCTCTC 123  
QY 150 GAACTCGAATTAATACCGCATAGCT--CTAGCGGAGAAAGCAGGGGNTATTAGACCTTG 208  
Db 124 GAAAGGAGCGCTAATACCGCATAGCTCTACCGGAGAAAGCAGGGGACCTTCGCGGCGCTG 183  
QY 209 CGCTATTAGATAGCTTAAGTCGGATTAGTAGTGGGTAAAGCCTTACCATGGCG 268  
Db 184 CGCTATCAGATGAGCTTACCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 243  
QY 269 ACAGTCTGATGCTGCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGCCGCGGA 328  
Db 244 ACAGTCCGTAATGCTGCTGAGAGGATGATCAGCTACACTGGAAGTACAGACGCTCCAGA 303  
QY 329 CT-CTAGCGGAGCAGTGGGGAATTTGGCAATATGNGGGAACCTGTATCCAGCAT 387  
Db 304 CTCCTAGGAGCAGCAGTGGGGAATTTGGCAATATGNGGGAACCTGTATCCAGCAT 363  
QY 388 GCGCGTGTGTAGNAGGCTTTTGGTGTAAAGCACTTTAGCACTGAGAGACTCT 447  
Db 364 GCGCGTGTGTAAAGAGGCTTCTCGGATTTAAAGCACTTTAAAGTGGGAGGAGGCAAT 423  
QY 448 TCGGTTAATACCGGGGAGGATGATGATGCTGAGAAATAGCACCGGCTAAGCTCTGTGC 507  
Db 1524 TC 1525

Db 424 TRACCTAATACCTAGTGTGTTTGAACGTACCGACAGATAGACCCGGCTACTCTGTGC 483  
 QY 508 CAGCAGCCGGGTAAATACAGAGGTGCAAGCGTTAAACGGAATTAATCTGAGCGGTAAAGCGA 567  
 Db 484 CAGCAGCCGGGTAAATACAGAGGTGCAAGCGTTAAACGGAATTAATCTGAGCGGTAAAGCGC 543  
 QY 568 GCGTAGGTGGTGTGATAGTCAGATCGAATCCCGGGCTTAACCTGGGAACTCACTCACT 627  
 Db 544 GCGTAGGTGGTGTGATAGTCAGATCGAATCCCGGGCTTAACCTGGGAACTCACTCACT 603  
 QY 628 GAACTGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGT 687  
 Db 604 AAACTGCAAGCTAGATGATGATGAGAGGTGAGATTTCTGTTGAGCGGTGAATG 663  
 QY 688 CGTAGAGATCTGAGGAAATACCGATGGGAGGAGCTTCTGTCATCACTGACATG 747  
 Db 664 CSTAGATATAGGAGGAACACCACTAGTGGCGAGGCGACCACTGGACCTGATCTGACATG 723  
 QY 748 AGGCTCGAAAGCGTGGGTAGCAACAGGATAGATACCTGTTAGTCCAGCGCGTAAACG 807  
 Db 724 AGTGGCAAGCGTGGGAGCAACAGGATAGATACCTGTTAGTCCAGCGCGTAAACG 783  
 QY 808 ATGCTACTAGTCTGGGTGCTTGGGTGCTTGGGTGCTTGGGTGCTTGGGTGCTTGGGTGCTTGG 867  
 Db 784 ATGCTAACTAGCGTGGGAGCTTGGGTGCTTGGGTGCTTGGGTGCTTGGGTGCTTGGGTGCTTGG 843  
 QY 868 CCGCTGGGAGTACGGCCGCAAGTTAAACTCAATGAATTCAGCGGGGCGCCGCAAA 927  
 Db 844 CCGCTGGGAGTACGGCCGCAAGTTAAACTCAATGAATTCAGCGGGGCGCCGCAAA 903  
 QY 928 CGGCTGGGAGTACGGCCGCAAGTTAAACTCAATGAATTCAGCGGGGCGCCGCAAA 987  
 Db 904 CGGCTGGGAGTACGGCCGCAAGTTAAACTCAATGAATTCAGCGGGGCGCCGCAAA 963  
 QY 988 CACAGAACTCTGAGAGATAGAGAGTGGCTTCGGGAAATTTGTATAGAGTGTGCTGATGG 1047  
 Db 964 CAATGAACCTTTCAGAGATGATGGGTGGCTTCGGGAAATTTGTATAGAGTGTGCTGATGG 1023  
 QY 1048 CTGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107  
 Db 1024 CTGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083  
 QY 1108 CTTAGTTACCAAGCA- TTCCGGTGGGAACTCTAAGGATGCTGCCAGTACCAACTGGAG 1166  
 Db 1084 CTTAGTTACCAAGCAAGTAAATGCTGGGCACTCTAAGGAGACTGCCGTGACAAACCGGAG 1143  
 QY 1167 GAGCGGGGAGCAGCTCAAGTCAATGATGCTTACGACGAGGCTTACAGAGTGTGCTGAT 1226  
 Db 1144 GAGGTTGGGATGAGCTCAAGTCAATGATGCTTACGACGAGGCTTACAGAGTGTGCTGAT 1203  
 QY 1227 AATGTTAGTACAGAGGCACTACAGAGGATGATGCTGGAATCTCAAAAGGCTATG 1286  
 Db 1204 AATGTTAGTACAGAGGTTGCCAAGCGGAGTGGAGCTAATCCCAAAACCGATG 1263  
 QY 1287 TACTCAGATGGAGTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 1346  
 Db 1264 TACTCAGATGGAGTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 1323  
 QY 1347 TCAGATGCGGGTGAATAGTTCGCGGCTTGTACACACGCGCGTTCACACCATGG 1406  
 Db 1324 TCAGATGCGGGTGAATAGTTCGCGGCTTGTACACACGCGCGTTCACACCATGG 1383  
 QY 1407 AGTTGATTCACCAAGTGTGTTAGCTAA-CTTAGTGGGCGGATCACACCGGTGTGT 1465  
 Db 1384 AGTGGTTCACCAAGTGTGTTAGCTAA-CTTAGTGGGCGGATCACACCGGTGTGT 1443  
 QY 1466 CGATGACTGGGTGAAGTCTGATACAGAGTGGGTAGGGGAACCTGGCGGTGATCAT 1523  
 Db 1444 TCATGACTGGGTGAAGTCTGATACAGAGTGGGTAGGGGAACCTGGCGGTGATCAT 1501

RESULT 13  
 AAI64998

ID AAI64998 standard; DNA; 1501 BP.  
 XX  
 AC AAI64998;  
 XX  
 DT 11-DEC-2001 (first entry)  
 XX  
 DE Polyhydroxyalkanoic acid related *Pseudomonas jessenii* coding sequence.  
 XX  
 KW Polyhydroxyalkanoic acid; PHA; biodegradable plastic; ds.  
 XX  
 OS *Pseudomonas jessenii*.  
 PN JP2001178484-A.  
 XX  
 PD 03-JUL-2001.  
 XX  
 PF 27-DEC-1999; 99JP-0371866.  
 XX  
 PR 27-DEC-1999; 99JP-0371866.  
 XX  
 PA (CANO ) CANON KK.  
 XX  
 DR WPI; 2001-592589/67.  
 XX  
 PT Microbial preparation of polyhydroxyalkanoic acids, using new carbon  
 PI sources useful as raw material for biodegradable plastics -  
 XX  
 PS Disclosure; Page 9; 10pp; Japanese.  
 XX  
 CC The present invention relates to the production of  
 CC polyhydroxyalkanoic acids. These can then be used in the production of  
 CC biodegradable plastics. The present sequence is a *Pseudomonas jessenii*  
 CC coding sequence described in the exemplification of the invention.  
 XX  
 SQ Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;  
 Query Match 72.0%; Score 1098.6; DB 22; Length 1501;  
 Best Local Similarity 85.9%; Pred. No. 0;  
 Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;  
 QY 30 GGGCGGAGGCTTACACATGCAAGTTCGCGGAAAGATGATGATGATGATGATGATGATGATGATGATGAT 89  
 Db 9 GGGCGGAGGCTTACACATGCAAGTTCGCGGAAAGATGATGATGATGATGATGATGATGATGATGATGAT 66  
 QY 90 GAGCNCGGAGGCTGAGTAATTAATAGTAATTAATAGTAATTAATAGTAATTAATAGTAATTAATAGTAAT 149  
 Db 67 G---CGCGGAGGCTGAGTAATTAATAGTAATTAATAGTAATTAATAGTAATTAATAGTAATTAATAGTAAT 123  
 QY 150 GAACTTCGGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCAATAGACCTTG 208  
 Db 124 GAAAGGAGCGCTAATACCGCATACGTCTACGGGAGAAAGCAGGGGACCTTCGGGCTTG 183  
 QY 209 CGCTATAGTACGCTTAAGTTCGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 268  
 Db 184 CGCTATAGTACGCTTAAGTTCGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 243  
 QY 269 ACATCTGTAGTGTCTGTAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 328  
 Db 244 ACATCTGTAGTGTCTGTAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 303  
 QY 329 CT-CTACGGGAGGAGAGTGGGGAATATTGGACAAATGNGNGGAAACCTGATCCAGCAT 387  
 Db 304 CTCCTACGGGAGGAGAGTGGGGAATATTGGACAAATGNGNGGAAACCTGATCCAGCAT 363  
 QY 388 GCGCGTGTGTGAAGAGGCTTTTGGTTGTAAGCACTTTAAGCAGTGTAAAGCACTGTAAAGCACTGT 447  
 Db 364 GCGCGTGTGTGAAGAGGCTTTTGGTTGTAAGCACTTTAAGCAGTGTAAAGCACTGTAAAGCACTGT 423  
 QY 448 TCGGTTAATATACCGGGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 507  
 Db 424 TACCTTAATACGTTAGTGTGTTTGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483  
 QY 508 CAGCAGCCGGGTAAATACAGAGGTGCAAGCGTTAAACGGAATTAATCTGAGCGGTAAAGCGA 567

Db 484 CACACCGCGGTAAATACAGAGGTGCACGCTTAATCGGAATACTGGCGCTAAGCGC 543  
QY 568 GCGTAGGTGGCTGTGAATAGTCAGATGTGAATCCCGGGCTTAACCTGGGAATCGATCT 627  
Db 544 GCGTAGGTGGCTGTGAATAGTCAGATGTGAATCCCGGGCTTAACCTGGGAATCGATCT 603  
QY 628 GBACTGTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 687  
Db 604 AARACTGACACTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 663  
QY 688 CGTAGAGATCTGAAGAAATACCGATGCGGAAGCAGCTTCCCTGGGCATCACTGACACTG 747  
Db 664 CGTAGATATAGGAAGAAACACCTAGCTGCGGAAGCAGCTTCCCTGGGCATCACTGACACTG 723  
QY 748 AGCTCGAAGCTGGGTAGCAAAACAGATTAATAGTACCTGCTAGTCCAGCGCTAAGCG 807  
Db 724 AGTGGCAAGCTGGGTAGCAAAACAGATTAATAGTACCTGCTAGTCCAGCGCTAAGCG 783  
QY 808 ATGTCTACTAGTCTGTGGTCCCTTGGAGCTTGTAGTACGAGCTTAAGCAATAGTGA 867  
Db 784 ATGTCAACTAGCTGTGGAGCTTGTAGTACGAGCTTGTAGTACGAGCTTGTAGTGA 843  
QY 868 CCGCCCTGGGAGTACGCGGCAAGGTTAAACTCAATGAATGACGCGGCGCGGCACAA 927  
Db 844 CCGCCCTGGGAGTACGCGGCAAGGTTAAACTCAATGAATGACGCGGCGCGGCACAA 903  
QY 928 GCGGTGACATGTGGTTAATTCATGCAACCGGAAGAACCTTACTGTGCTTGGACATA 987  
Db 904 GCGGTGACATGTGGTTAATTCATGCAACCGGAAGAACCTTACTGTGCTTGGACATA 963  
QY 988 CACAGAACTCTGTAGAGTACAGAGTGCCTTCGGGAATGTGTACAGAGTGTGATG 1047  
Db 964 CATGTAACTTCCAGAGATGATGGTGCCTTCGGGAATGTGTACAGAGTGTGATG 1023  
QY 1048 CTGTCTGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107  
Db 1024 CTGTCTGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083  
QY 1108 CTTTGTACAGCTAC- TTCGGGTGGGAATCTTAAGTACGAGCTTACGAGTACAGCTGAG 1166  
Db 1084 CTTTGTACAGCTAC- TTCGGGTGGGAATCTTAAGTACGAGCTTACGAGTACAGCTGAG 1143  
QY 1167 GAAGGCGGAGCTACGCTACGCTACGCTACGCTACGCTACGCTACGCTACGCTACG 1226  
Db 1144 GAAGGCGGAGCTACGCTACGCTACGCTACGCTACGCTACGCTACGCTACGCTACG 1203  
QY 1227 AATGCTAGCTACAGAGGCTACGCTACGCTACGCTACGCTACGCTACGCTACGCTACG 1286  
Db 1204 AATGCTAGCTACAGAGGCTACGCTACGCTACGCTACGCTACGCTACGCTACGCTACG 1263  
QY 1287 TAGTCCAGATGTGAGTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1346  
Db 1264 TAGTCCAGATGTGAGTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1323  
QY 1347 TCAGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1406  
Db 1324 TCAGATGCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1383  
QY 1407 AGTTGATGTCACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1465  
Db 1384 AGTGGGTGTCACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1443  
QY 1466 CGATGCTGGGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1523  
Db 1444 TCATGACTGGGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1501

RESULT 14  
AAH77497  
ID AAH77497 standard; DNA; 1501 BP.  
XX  
AC AAH77497;

XX 20-NOV-2001 (first entry)  
DT Pseudomonas jessenii P161 coding sequence fragment.  
XX Polyhydroxyalkanoate; PHA; ds.  
KW Pseudomonas jessenii.  
OS JP2001178485-A.  
XX 03-JUL-2001.  
PD 27-DEC-1999; 99JP-0371865.  
XX 27-DEC-1999; 99JP-0371865.  
PR (CANO ) CANON KK.  
XX WPI; 2001-586288/66.  
DT Production of a polyhydroxyalkanoate useful as a functional polymer -  
PT Disclosure; Page 9; 12pp; Japanese.  
PS The present invention describes a method of producing a  
XX polyhydroxyalkanoate (PHA) using a microbe. This may be Pseudomonas  
CC cichorii YN2, Pseudomonas cichorii H45 or Pseudomonas jessenii P161. The  
CC PHA produced using the method of the invention is useful as a functional  
CC polymer. The present sequence is a fragment of the P. jessenii coding  
CC sequence.  
XX Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;  
SQ Query Match 72.0%; Score 1098.6; DB 22; Length 1501;  
Best Local Similarity 85.9%; Pred. No. 0;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

QY 30 GCGCGGAGGCTTACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 89  
Db 9 GCGCGGAGGCTTACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 66  
QY 90 GAGCNGCGGAGGCTTACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 149  
Db 67 G---CGCGGAGGCTTACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 123  
QY 150 GAAACTCGAATTAATACCGCATAGCT-CTAGCGGAGAAAGCAGGGGNTCACTAGACCTTG 208  
Db 124 GAAAGGAGCGCTAATACCGCATAGCT-CTAGCGGAGAAAGCAGGGGNTCACTAGACCTTG 183  
QY 209 CGCTATTAGATGAGCTTACCGCATAGCT-CTAGCGGAGAAAGCAGGGGNTCACTAGACCTTG 268  
Db 184 CGCTATTAGATGAGCTTACCGCATAGCT-CTAGCGGAGAAAGCAGGGGNTCACTAGACCTTG 243  
QY 269 ACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 328  
Db 244 ACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 303  
QY 329 CT-CTAGCGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 387  
Db 304 CTCCTAGCGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 363  
QY 388 GCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 447  
Db 364 GCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 423  
QY 448 TCGGTTAATACCGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 507  
Db 424 TAACTTAATACCGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 483  
QY 508 CAGCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 567  
Db 484 CAGCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 543

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QY 568 GCCTAGTGGCTGTGATAGTCAATGTAATCCCGGGCTTAACCTGGGAATCTCATCT 627
Db 544 GCCTAGTGGCTGTGATAGTCAATGTAATCCCGGGCTTAACCTGGGAATCTCATCT 603
QY 628 GAACTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT 687
Db 604 AATCTGACAGCTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT 663
QY 688 CSTAGATCTGTAGGAAATACCATGCGGAGGCGAGTCTCTGCGATCATATGACATG 747
Db 664 CSTAGATATAGGAGGAACACAGTGTGCGAGGCGAGGCGAGTCTCTGCGATCATATG 723
QY 748 AGCTCTGAAAGCTGGTGTGCAACACAGGATTAATGATACCTGTGTGCGGCGGTAACG 807
Db 724 AGTGTGAAAGCTGGTGTGCAACACAGGATTAATGATACCTGTGTGCGGCGGTAACG 783
QY 808 ATCTCTACTAGTCTGTGGTCCCTTACGAGCTTACTGACGAGTACGCAATAGTAGA 867
Db 784 ATCTCACTAGCCTTGGAGCCTTGTAGTCTTACTGCGCAGCTAACGCAATAGTTGA 843
QY 868 CGCCTGTGGAGTACGCGCGGAGGTTAAACTCAATGATGACGGGGCGCGCAAA 927
Db 844 CGCCTGTGGAGTACGCGCGGAGGTTAAACTCAATGATGACGGGGCGCGCAAA 903
QY 928 CGGTGTGAGCATGTGTTTAAATTCGATGCAACGCGGAACCTTACCTGTGTGTGACATA 987
Db 904 CGGTGTGAGCATGTGTTTAAATTCGATGCAACGCGGAACCTTACCTGTGTGTGACATA 963
QY 988 CACAGAACTTGTAGAGTACGAGTGTGCTTTCGGGAAATGTGATACAGTGTGCTCAGG 1047
Db 964 CAATGAACCTTTCAGAGTGTGAGTGTGCTTTCGGGAAATGTGATACAGTGTGCTCAGG 1023
QY 1048 CTGTCTGACGTCTGCTGAGATGTGCTTGTGATGCTCCGACGAGCGCAACCTGT 1107
Db 1024 CTGTCTGACGTCTGCTGAGATGTGCTTGTGATGCTCCGACGAGCGCAACCTGT 1083
QY 1108 CTTAGTTACCAAGC-TTCCGGTGGGAATCTAAGGATCTGCGAGTACGCAATCTGGAG 1166
Db 1084 CTTAGTTACCAAGCAGTAAATGGTGGCACTCTAAGGAGTCTCCGCTGACAAACCGGAG 1143
QY 1167 GAGGCGGGAGCAGTCAATGATCATGCGCCCTTACACAGGCTTACACAGTGTGCTAC 1226
Db 1144 GAAGGTGGGAGTCAATGATCATGCGCCCTTACGCGCTGGGCTTACACAGTGTGCTAC 1203
QY 1227 AATGGTAGTACAGAGGCGAGTACACAGGATGTGATCGGAATCTCAAAAGCCTATCG 1286
Db 1204 AATGGTAGTACAGAGGCTTCCAGCGCGGAGTGTGAGTAACTCCACAAACCGATCG 1263
QY 1287 TAGTCCAGATTGAGTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 1346
Db 1264 TAGTCCGGATGCGAGTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 1323
QY 1347 TCAGATGCGGGGTGAATAGTCTGCGGGCTTGTACACACCGCGCTGACACACATGGG 1406
Db 1324 TCAGATGCGGGGTGAATAGTCTGCGGGCTTGTACACACCGCGCTGACACACATGGG 1383
QY 1407 AGTTGATTCACAGAGTGTGTAGCTAA-CTTAGTGGGGCGGATCACCACGGTGTGT 1465
Db 1384 AGTGGTTCACAGAGTGTGTAGCTAACTTACCTTCCGGAGGAGGTTAOCACGGTGTGT 1443
QY 1466 GATGACTGGGTGAAGTCGTAACAGGATGCGGTAGGGGAACCTGCGGTGTGTATC 1523
Db 1444 TCATGACTGGGTGAAGTCGTAACAGGATGCGGTAGGGGAACCTGCGGTGTGTATC 1501
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RESULT 15

AAS12097

ID AAS12097 standard; DNA; 1501 BP.

XX

AC AAS12097;

XX

DT 21-NOV-2001 (first entry)

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XX Pseudomonas jessenii 161 strain.
XX Polyhydroxyalkanoate; alkanolate; microorganism; functional polymer; ds;
XX medical material.
XX Pseudomonas jessenii.
OS
XX EP1113033-A2.
XX 04-JUL-2001.
XX 22-DEC-2000; 2000EP-0128444.
XX 27-DEC-1999; 99JP-0371863.
PR 31-JAN-2000; 2000JP-0023078.
PR 31-JAN-2000; 2000JP-0023080.
PR 31-JAN-2000; 2000JP-0023083.
PR 30-MAR-2000; 2000JP-0095011.
PR 30-MAR-2000; 2000JP-0095012.
PR 30-MAR-2000; 2000JP-0095013.
PR 07-JUL-2000; 2000JP-0207089.
PR 07-JUL-2000; 2000JP-0207091.
PR 27-NOV-2000; 2000JP-0359789.
XX (CANO ) CANON KK.
XX Honma T, Kobayashi T, Yano T, Kobayashi S, Inamura T, Suda S;
PI Kenmoku T;
XX WPI; 2001-537748/60.
XX New polyhydroxyalkanoates useful as functional polymers e.g. in medical
XX devices
XX Claim 36; Page 83-84; 184pp; English.
XX The invention relates to polyhydroxyalkanoates comprising monomer units
XX of diverse structures containing side chain substituents. This sequence
XX represents a Pseudomonas jessenii 161 strain microorganism, capable of
XX synthesising a polyhydroxyalkanoate from an alkanolate. By culturing a
XX microorganism in a medium containing an alkanolate, a polyhydroxyalkanoate
XX can be obtained. Polyhydroxyalkanoates are used as functional polymers,
XX particularly in medical devices and materials. The use of microorganisms
XX yields polymers of high purity and in high yield.
XX Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;
```

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Query Match 72.08; Score 1098.6; DB 22; Length 1501;
Best Local Similarity 85.94; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;
QY 30 GCGGCGAGCTTAACACATGCAATGCGAGCGGAACGATGATGCTGTATATAGGCGTC 89
Db 9 GCGGCGAGCTTAACACATGCAATGCGAGCGG-ATGACGGGAGCTTGTCTCTGATTTCA 66
QY 90 GAGCNCOCGAGCGGTGAGTAACTAGTAACTAGTAACTAGTAACTAGTAACTAGTAACTAG 149
Db 67 G--CGGCGAGCGGTGAGTAACTAGTAACTAGTAACTAGTAACTAGTAACTAGTAACTAG 123
QY 150 GAACTCAATTAATACCGATACGT-CTACGGGAGAAACGAGGGGNTCATTAGACCTTG 208
Db 124 GAAAGGAGCGTAAATACCGATACGTCTACGGGAGAAACGAGGGGACCTTGGGCGCTTG 183
QY 209 CGCTATTAGATGACCTTAAGTCGATTAGTGTGGGTAAAGGCTTACCATGCGG 268
Db 184 CGCTATCAGATGACCTTAGTGTGGGTAAAGGCTTACCATGCGG 243
QY 269 ACATCTCTAGTGTCTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 328
Db 244 ACATCTCTAGTGTCTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 303
QY 329 CT-CTACGGGAGGAGCAGTGGGGATATTTGACAAATGGGGAACCCCTGATCCAGCAT 387
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Db	304	388	364	448	424	508	484	568	544	628	604	688	664	748	724	808	784	868	844	928	904	988	964	1048	1024	1108	1084	1168	1144	1228	1204	1288	1264	1348	1324	1408	1407
Db	363	447	423	507	483	567	543	627	603	687	663	747	723	807	783	867	843	927	903	987	963	1047	1023	1107	1083	1166	1143	1226	1203	1286	1263	1346	1323	1406	1383	1465	
QY	363	447	423	507	483	567	543	627	603	687	663	747	723	807	783	867	843	927	903	987	963	1047	1023	1107	1083	1166	1143	1226	1203	1286	1263	1346	1323	1406	1383	1465	
Db	363	447	423	507	483	567	543	627	603	687	663	747	723	807	783	867	843	927	903	987	963	1047	1023	1107	1083	1166	1143	1226	1203	1286	1263	1346	1323	1406	1383	1465	
QY	363	447	423	507	483	567	543	627	603	687	663	747	723	807	783	867	843	927	903	987	963	1047	1023	1107	1083	1166	1143	1226	1203	1286	1263	1346	1323	1406	1383	1465	
Db	363	447	423	507	483	567	543	627	603	687	663	747	723	807	783	867	843	927	903	987	963	1047	1023	1107	1083	1166	1143	1226	1203	1286	1263	1346	1323	1406	1383	1465	
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Db	363	447	423	507	483	567	543	627	603	687	663	747	723	807	783	867	843	927	903	987	963	1047	1023	1107	1083	1166	1143	1226	1203	1286	1263	1346	1323	1406	1383	1465	
QY	363	447	423	507	483	567	543	627	603	687	663	747	723	807	783	867	843	927	903	987	963	1047	1023	1107	1083	1166	1143	1226	1203	1286	1263	1346	1323	1406	1383	1465	
Db	363	447	423	507	483	567	543	627	603	687	663	747	723	807	783	867	843	927	903	987	963	1047	1023	1107	1083	1166	1143	1226	1203	1286	1263	1346	1323	1406	1383	1465	
QY	363	447	423	507	483	567	543	627	603	687	663	747	723	807	783	867	843	927	903	987	963	1047	1023	1107	1083	1166	1143	1226	1203	1286	1263	1346	1323	1406	1383	1465	
Db	363	447	423	507	483	567	543	627	603	687	663	747	723	807	783	867	843	927	903	987	963	1047	1023	1107	1083	1166	1143	1226	1203	1286	1263	1346	1323	1406	1383	1465	
QY	363	447	423	507	483	567	543	627	603	687	663	747	723	807	783	867	843	927	903	987	963	1047	1023	1107	1083	1166	1143	1226	1203	1286	1263	1346	1323	1406	1383	1465	
Db	36																																				



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OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 01:43:45 ; Search time 3470.79 seconds  
(without alignments)  
10685.946 Million cell updates/sec

Title: US-09-979-558a-1  
Perfect score: 1526  
Sequence: 1 ttgatcatcggtccagatt.....acctgcggtgatcacctc 1526

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

EST.\*

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estnu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_htc.\*

9: gb\_esti.\*

10: gb\_est2.\*

11: gb\_htc.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

19: em\_gss\_pln.\*

20: em\_gss\_vrt.\*

21: em\_gss\_fun.\*

22: em\_gss\_mam.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rod.\*

26: em\_gss\_pbg.\*

27: em\_gss\_vrl.\*

28: gb\_gssi.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Score	Match Length	ID	Description
1	851	55.8	6499	28 BH771024
2	617	40.4	1084	29 B2439740
3	616.8	40.4	1054	28 BH647750
4	606.8	39.8	1044	29 B2463550

C 5	606.8	39.8	1051	29 B2494182
C 6	606.6	39.8	1053	29 B2447500
C 7	603.6	39.6	1010	29 B2431523
C 8	602.6	39.5	1031	28 BH656222
C 9	600.4	39.3	1077	29 B2450751
C 10	595.2	39.0	1016	29 B2426201
C 11	591.8	38.8	1079	28 BH705272
C 12	582.4	38.2	741	14 CD042372
C 13	571.6	37.5	1143	28 BH814966
C 14	571.6	37.4	974	29 B2440868
C 15	562	36.8	951	28 BH651765
C 16	557.4	36.5	1096	29 B2502068
C 17	556.4	36.5	901	29 B2461852
C 18	552.6	36.2	977	29 B2459292
C 19	552.4	36.2	1068	29 B2576668
C 20	549	36.0	899	29 B2685785
C 21	548.6	36.0	918	29 B2437960
C 22	548.4	35.9	699	14 CD043647
C 23	547.2	35.9	1010	29 B2568539
C 24	545	35.7	1205	29 B2566538
C 25	542	35.5	947	29 B2464837
C 26	540.6	35.4	1069	29 B2474941
C 27	537.8	35.2	674	14 CD044496
C 28	535.6	35.1	1030	29 B2463792
C 29	533	34.9	641	14 CD040169
C 30	533	34.9	943	29 B2468986
C 31	531.2	34.8	1106	29 B2469058
C 32	527.8	34.6	981	29 B2442959
C 33	524.4	34.4	873	28 BH705306
C 34	522.4	34.2	882	29 B2455326
C 35	519.2	34.0	837	29 B2483676
C 36	518.6	34.0	846	28 BH562180
C 37	518.2	34.0	842	28 BH482629
C 38	517.8	33.9	862	28 BH527452
C 39	516.6	33.9	953	29 B2440283
C 40	515.2	33.8	831	29 B2501502
C 41	514.4	33.7	835	28 BH552149
C 42	514.2	33.7	889	29 B2428275
C 43	511.6	33.5	848	28 BH535640
C 44	511	33.5	822	29 B2446240
C 45	511	33.5	882	29 B2499755

#### ALIGNMENTS

RESULT 1	BH771024	6499 bp	DNA	linear	GSS 01-MAY-2002
LOCUS	LLMGTAG746	MG1363	Random Sequence Tag Library	Lactococcus lactis	
DEFINITION	subsp. cremoris genomic, genomic survey sequence.				
ACCESSION	BH771024				
VERSION	BH771024.1				
KEYWORDS	GSS.				
SOURCE	Lactococcus lactis subsp. cremoris				
ORGANISM	Lactococcus lactis subsp. cremoris				
REFERENCE	1 (bases 1 to 6499)				
AUTHORS	Bolotin,A., Ehrlich,S.D. and Sorokin,A.				
TITLE	Studies of genomes of dairy bacteria Lactococcus lactis				
JOURNAL	Sci. Aliments, (2002) in press				
COMMENT	Contact: sorokin A Genetique Microbienne INRA CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France Tel: 33 1 34 65 25 16 Fax: 33 1 34 65 25 21 Email: sorokine@jouy.inra.fr best homologue in strain ILL403 is ywga (78%) Class: shotgun High quality sequence start: 30 High quality sequence stop: 6471.				



FEATURES  
source

Location/Qualifiers  
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/organism="Lactococcus lactis subsp. cremoris"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:1359"  
/clone\_lib="MG1363 Random Sequence Tag Library"  
/note="Vector: pSGM2; Site 1: SmaI; Library of  
chromosomal fragments of L. lactis strain MG1363 was  
prepared by partial AluI digestion or by sonication."  
BASE COUNT 1946 a 1228 c 1683 g 1642 t  
ORIGIN

Query Match 55.8%; Score 851; DB 28; Length 6499;  
Best Local Similarity 75.4%; Pred. No. 1.8e-225;  
Matches 1137; Conservative 0; Mismatches 358; Indels 13; Gaps 6;

QY 30 GGGGAGGCTTAACACATGCAAGTCGAGCGGAACATGATAGTCTGCTATTAGGCTC 89  
DB 562 GGGGGCTGCTTAATACATGCAAGTTGAGCGATGAAGATTGCTTGCACCAATTGAA 621  
QY 90 GAGCNGCGGACGGGTGAGTATATCTTAGGAATCTACCTACTAGTGGGGTAGCTCGG 149  
DB 622 GAGCAGCGAAGCGGTGAGTAAAGCGGTGGGAATCTGCCCTTGAGCGGGGGAACAATTG 681  
QY 150 GAAACTCGAATTAATACCGCATAGCTCTACGGGAGA-----AAGCAGGGGNTCATTA 201  
DB 682 GAAACGAATGCTAATACCGCATATACTTTAAACATAAGTTTAAAGTTTGAAGATGCA 741  
QY 202 GACCTTCGCTATAGATAGAGCTTAAGTCGGATTAGCTAGATGTTGGGGTAAAGGCTAC 261  
DB 742 ATTGCATCACTAAAGATGATCCCGCGTTCTATTAGCTAGTGGTGGTAGTAAGGCTAC 801  
QY 262 CATGGCAGCATCTGATGATGCTGTGAGAGGATGATCAGCACACCGGACCTGAGACAG 321  
DB 802 CRAAGCGATACATAGCCGACCTTGAGAGGCTGATCGGCCACATGCGGACTGAGACAG 861  
QY 322 GCCCGGACT-CTACGGGAGCAGCAGTGGGGAATATTGGACAATGNGGGAACCCCTGATC 380  
DB 862 GCCCAAACTCTACGGGAGCAGCAGTAGGGAATCTCGCAATGGACAAAGCTGAC 921  
QY 381 CAGCCATGCCGCTGTGTGAAGAGCGCTTTGGTGTAAAGCACTTTAAGCAGTGAAGA 440  
DB 922 GAGCAACGCCGCTGAGTGAAGAGGTTTCGGATCGTAAACTCTGTGTGTAGAGAAGA 981  
QY 441 A-GACTCTCTGCTTAAATACCGGACGATGACATAGCTGACAGATAAGCACCGGCTAA 499  
DB 982 ACGTGTGTGAGGTGAAGAGCTCATCAAGTGACGCTAATCACTCCCAAGAAAGGCGGCTAA 1041  
QY 500 CTCGTGCCAGCAGCCGGTAAATACAGAGGTCGACAGGTTAATCGGAATTACTGGGCG 559  
DB 1042 CTACGTGCCAGCAGCCGGTAAATAGCTAGTGTCCGAGCGTTGTCGGATTTATTGGGCG 1101  
QY 560 TAAAGCAGCGTAGTGGCTTGAATGATGATGATGATGATGATGATGATGATGATGATG 619  
DB 1102 TAAAGCAGCGTAGTGGCTTGAATGATGATGATGATGATGATGATGATGATGATGATG 1161  
QY 620 CTGCATCTGAACTCTGAGCTAGATGATGATGATGATGATGATGATGATGATGATGATG 679  
DB 1162 TGCATGGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1220  
QY 680 GTGAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 739  
DB 1221 GTGAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1280  
QY 740 TGACACTGAGGCTCGAAGCGGTGAGTGAAGCAACAGATGATGATGATGATGATGATGAT 799  
DB 1281 TGACACTGAGGCTCGAAGCGGTGAGTGAAGCAACAGATGATGATGATGATGATGATGAT 1340  
QY 800 CGTAAAGAGTGTACTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 859  
DB 1341 CGTAAAGAGTGTACTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1400

QY 860 TAAGTAGACCGCTGGGAGTAGCGCGCAAGCTAAATCTAAATCTAAATCTAAATCTAAATCT 919  
DB 1401 TAGCACTCGGCTGGGAGTAGCGCGCAAGCTAAATCTAAATCTAAATCTAAATCTAAATCT 1460  
QY 920 CCGCACAGCGGTGGAGCATGTGTTTAAATCTAAATCTAAATCTAAATCTAAATCTAAATCT 979  
DB 1461 CCGCACAGCGGTGGAGCATGTGTTTAAATCTAAATCTAAATCTAAATCTAAATCTAAATCT 1520  
QY 980 TTGACATACACAGATCTTGTAGAGATACGAGAGTCCCTCGGGAATCTGTGATACAGGTG 1039  
DB 1521 TTGACATACACAGATCTTGTAGAGATACGAGAGTCCCTCGGGAATCTGTGATACAGGTG 1580  
QY 1040 CTGCATGGGTCTGCTCAGCTGCTGCTGAGATGTTGGGTAAAGTCGCGCAACGACGCA 1099  
DB 1581 GTGCATGGGTCTGCTCAGCTGCTGCTGAGATGTTGGGTAAAGTCGCGCAACGACGCA 1640  
QY 1100 ACCCTTGTCTTGTAGTACACACTTCCGTTGGGAATCTTAAGATATCTGCTAGTACAA 1159  
DB 1641 ACCCTTGTCTTGTAGTACACACTTCCGTTGGGAATCTTAAGATATCTGCTAGTACAA 1699  
QY 1160 ACTGGAGGAGCGGGGAGCAGCTCAAGTCATCATCGCTTACGACAGGCTACACAC 1219  
DB 1700 ACCGAGGAGGTGGGGATGACGTCRAATCATCTCTCCCTTAAGCTTGGGTACACAC 1759  
QY 1220 GTGCTACAATGGTAGTACAGAGGCGAGCTACACAGCGATGTGATGCGAATCTCAAAAAG 1279  
DB 1760 GTGCTACAATGGTAGTACAGAGGCGAGCTACACAGCGATGTGATGCGAATCTCAAAAAG 1819  
QY 1280 CTTATCGTAGTCCAGATGGAGTCTGCACTCGACTCCATGATGATGATGATGATGATGAT 1339  
DB 1820 CTTATCGTAGTCCAGATGGAGTCTGCACTCGACTCCATGATGATGATGATGATGATGAT 1879  
QY 1340 TCGCGGATCAGATGCGCGGTGAATAGCTTCCCGGCTTGTACACACCGCGCTCAACA 1399  
DB 1880 TCGCGGATCAGACGCGCGGTGAATAGCTTCCCGGCTTGTACACACCGCGCTCAACA 1939  
QY 1400 CCATGGGAGTGAATGACACAGAGTGTGATGCTAA-CTTAGTGAGGGGAGTACACACG 1458  
DB 1940 CCAGGGAGTGGGAGTACCCGAAAGTAGTTCCTAACCGCAAGGAGGCGCTTCCTTAAG 1999  
QY 1459 GTGTGCTGACTGCTGGGTGAGTCTGATGATGATGATGATGATGATGATGATGATGATG 1518  
DB 2000 GTTAGACCGGATGCTGGGTGAGTCTGATGATGATGATGATGATGATGATGATGATGAT 2059  
QY 1519 ATCACCTC 1526  
DB 2060 ATCACCTC 2067

RESULT 2  
BZ439740  
LOCUS  
DEFINITION  
BOND54TF BO.1.6\_2\_KB\_tot Brassica oleracea genomic clone BOND54,  
genomic survey sequence.  
ACCESSION  
VERSION  
BZ439740.1  
GI:26695676  
KEYWORDS  
SOURCE  
Brassica oleracea  
ORGANISM  
Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids II; Brassicales; Brassicaceae; Brassica.  
REFERENCE  
1 (bases 1 to 1084)  
TOWN,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.  
Whole genome shotgun sequencing of Brassica oleracea  
Unpublished  
Other\_GSSs: BOND54TR  
Contact: Chris Town  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TF  
Class: sheared ends.

Location/Qualifiers

## FEATURES

source

1. .1084  
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/strain="Tol1000DH3"  
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/clone="BOMND31"  
/clone\_lib="BO.1.6.2.kb\_tot"  
/note="Vector: pHS1; Site 1: BstXI; 1.6-2 kb sheared  
total DNA inserted into pHS1 using BstXI linkers"

BASE COUNT

272 a 264 c 346 g 202 t

ORIGIN

Query Match 40.4%; Score 617; DB 29; Length 1084;

Best Local Similarity 76.3%; Pred. No. 1.1e-160;

Matches 832; Conservative 0; Mismatches 231; Indels 27; Gaps 5;

QY 258 CTACCATGCGGACGATCTGTAGCTGTCTGAGAGGATGATCAGCCACACCGGACTGAGA 317

Db 3 CTTACCGCGATGATCAGTACGTAGCTGTCGAGAGGA-GATCAGCCACACTGGGACTGAGA 61

QY 318 CACGGCCCGGACT-CTACGGAGGCGACGATGGGGAATATTGGACATGGNGGAACCT 376

Db 62 CACGGCCCGGACTCTCTACGGAGGCGACGATGGGGAATTTCCGCAATGGCGAAGCCT 121

QY 377 GATCCAGCCATCCCGCTGTGTGAAGAGCCCTTTTGTGTAAGACACTTTTAAGCAGTG 436

Db 122 GACGGAGCAATCCCGCTGGAGGTAGAAGCCCTACGGCTCTGAATCTTTCCAGAG 181

QY 437 AGAAGACTCTTCGGTTAATACCGGGGACGATGATGATGATGATGATGATGATGATGATG 496

Db 182 AAGAAG-----CAATGACGGTATCTGGGGAATTAAGCAATGACCGCG 218

QY 497 TAACCTGTGCGCAGCAGCCGGTAATACAGAGGGTGAAGGTTAATCGAATTAAGTGG 556

Db 219 TAACCTGTGCGCAGCAGCCGGTAATACAGAGGGTGAAGGTTAATCGAATTAAGTGG 278

QY 557 GCCTAAAGCGAGCGTAGTGGCTTGAATGATGATGATGATGATGATGATGATGATGATG 616

Db 279 GCCTAAAGCGCTGTAGTGGCTTTTAACTCGCGCTCAATCCAGGGCTCAACCGTC 338

QY 617 GAACCTGATCTGAACCTGTTAGCTAGATGATGATGATGATGATGATGATGATGATGATG 676

Db 339 GACAGCGGTGGAACTACCACTGATGATGATGATGATGATGATGATGATGATGATGATG 398

QY 677 GCGTGAATGCTAGATCTGAAGTAATACCGATGCGGAGGAGGAGGAGGAGGAGGAGGAG 736

Db 399 GCGTGAATGCTAGATCTGAAGTAATACCGATGCGGAGGAGGAGGAGGAGGAGGAGGAG 458

QY 737 TACTGACTGAGCGTCCGAACCGTGGGTAGCAACAGGATGATGATGATGATGATGATGATG 796

Db 459 CACTGACTGAGAGACGAAAGCTAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 518

QY 797 GCGGTAAACGATGCTACTAGTCTGTGGTCCCTGAGGACT-TAGTGAGCAGGACTAAC 855

Db 519 AGCCGTAAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 578

QY 856 GCAATAGTAGCCCGCTGGGAGTACGCCGCAAGGTTAAACATCAATGATGATGATGATG 915

Db 579 GCGTTAGTATCCCGCTGGGAGTACGTTCCGAGAATGAACTCAAGGAATGATGATGATG 638

QY 916 GGGCCCGCACAACGCGGTGAGCATGTGTTAATTCGATGCAACGCGAAGAACCTTACCT 975

Db 639 GGGCCCGCACAACGCGGTGAGCATGTGTTAATTCGATGCAACGCGAAGAACCTTACCA 698

QY 976 GGTCTTGACATACACAGAACTTGTAGAGATGAGAGTGCCTTCGGGAATGTGATFACA 1035

Db 699 GGGCTTGACATGCGCGAATCTCTTGAAGAGAGAGGGGTGCCTTCGGGAACGCGGACACA 758

QY 1036 GGTGCTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1095

Db 759 GGTGGTGCATGGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 818

QY 1096 CGCAACCCCTTGTCTTACTTACAGACACTTCGGGTGGGAACCTTAAGGATATCTCCAGTG 1155

Db 819 CGCAACCCCTTGTCTTACTTACAGACACTTCGGGTGGGAACCTTAAGGATATCTCCAGTG 877

QY 1156 ACAACTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1215

Db 878 ATAAGCCGGAGGAAGTGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 937

QY 1216 ACACGTGCTACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1275

Db 938 ACACGTGCTACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 997

QY 1276 AAAGCCTATGCTAGTCCAGATTGGAGTCTGCAACTCGACTCCATGATGATGATGATGATG 1335

Db 998 AAACCCGTCCTCAGTCGGATTGCGAGCTGCAACTCGACTCCATGATGATGATGATGATG 1057

QY 1336 GTAATCGCGG 1345

Db 1058 GTAATCGCGG 1067

## RESULT 3

BH647750/c

LOCUS

DEFINITION

ACCESION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1. .1054

/organism="Brassica oleracea"

/mol\_type="genomic DNA"

/strain="Tol1000DH3"

/db\_xref="taxon:3712"

/clone="BOMND31"

/clone\_lib="BO.2.3\_KB"

/note="Vector: pHS1; Site 1: BstXI; 2-3 kb sheared

genomic DNA inserted into pHS1 using BstXI linkers"

BASE COUNT

201 a 334 c 263 g 256 t

ORIGIN

Query Match

Best Local Similarity

Matches

808; Conservative

40.4%; Score 616.8; DB 28; Length 1054;

Pred. No. 1.3e-160;

Mismatches 227; Indels 5; Gaps 5;

QY 487 AAGCACCGGTTACTCTGTGCGCAGCAGCCGCGGTATATACAGAGGGTGCACCGTTATCG 546

Db 1054 AAGCATCGGTTACTCTGTGCGCAGCAGCCGCGGTATATACAGAGGGTGCACCGTTATCG 995

QY 547 GAATTAATCTGGCGTAAAGCGAGCGTAGTGGCTTGTATAAGTCAGATGTGAATCCCGGG 606

D	b	994		GAAATGATTGGCGCTAAAACGGTCTGTAGTGGGTTT-TTAAGTCCGCCGTCAAAATCCCAGG	936	
Q	y	607	C	T	TAAACTCGGGAACTCGATCTGAAACTGTTAGCCTAGAGTAGGTAGAGAGGGAAGTAGAAT	666
D	b	935	C	T	CACCCCTGGACAGCGCGTGGAAACTACCRAGCTTGASTAACGGTAGGGGCAGAGGGAAT	876
Q	y	667	T	T	CAGGTAGCGGTGAAATGGGTAGAGATCTGAAGGAATACCGATGGCGGAAGGCAAGCTT	726
D	b	875	T	T	CGGTGGAGCGGTGAAATGGGTAGAGATCGGAAGAACCACCAACCGCGGAAGCACTCT	816
Q	y	727	C	T	TGGCATCTACTCACACTGAGGCTCGAAAGCGTGGGTAGCAAAACAGGATTAGATACCC	786
D	b	815	G	C	TGGGCGCACACTGACACTGAGAGACGAAAGCTAGGGGACGGAATGGGATTTAGATACC	756
Q	y	787	T	G	TAGTCCACGCGTAAACGATGTCTACTAGTCTGTGGTGGTCCCTTGAGGACT- TAGTGA	845
D	b	755	C	A	GTAGTTCCTAGCCGTAAACGATGGATCTAGCGCTTGGGTATCGACCCCTGCAGTGC	696
Q	y	846	O	G	CAGCTAACGCAATAAGTAGACGGCTGGGAGTAGCGCGGCAAGTTAAACATCAAT	905
D	b	695	T	G	TAGTAAACGGCTTAAGTATCCCGCTGGGAGTAGCTTCGCAAGAATAAACAATCAAAG	636
Q	y	906	G	A	ATTGACGGGGCCCCACAAACGGGTGGAGCATGTGGTTTTAAITCGATGCAACCGCAAG	965
D	b	635	G	A	ATTGACGGGGCCCCACAAACGGGTGGAGCATGTGGTTTTAAITCGATGCAAAAGCGAAG	576
Q	y	966	A	A	CTTACCTTGCTTTGACATACACAGATCTTTGAGAGATACGAGAGTGCCCTTCGGGAA	1025
D	b	575	A	A	CTTACCAAGGSCTTGACATGCCCGCAATCTCTTGAAGAGNAGGGTGCCTTCGGGA	516
Q	y	1026	T	T	TGATACAGTGTCTGAWGCGTGTGTCAGCTCGTGTGTGAGATGTGGTTAAATC	1085
D	b	515	C	G	CGACACAGGTGTGATGGCTGTGCTGACGTGCTCCGTAAAGTGTGGTTAAATC	456
Q	y	1086	C	C	CACAGAGCGCAACCTTCTCTTAGTTTACACACATCTCGGTTGGGHACTCTAAGAT	1145
D	b	455	C	C	CACAGAGCGCAACCTTCTCTTAGTTTATGTCGA-CGFTTAGTTTGGAAACCTGAACAG	397
Q	y	1146	A	C	TGCCAGTACAAACTGGAGGAGCGGGAGCGCTCAAGTCATCATGGCCCTTACGA	1205
D	b	396	A	C	TCCGCTGATAAGCCGAGGAGGTGAGATGACGTCAGTCATCATGCCCTTATGC	337
Q	y	1206	C	A	GSGCTACACACGTGTCAATGTGWAAGTACAGAGGCGAGCTPACACAGAGCTGTGATG	1265
D	b	336	C	T	GGGCGACACACGTGTCAATAAGCCGSGCAAAAGGTCGCGATCCCGAGGGTGTAG	277
Q	y	1266	G	C	AAATCTAAAAAGCCTATCGTAGTTCAGATTGGAGTCTGCAACTGACTCCATGAAGTA	1325
D	b	276	C	T	AATCTCAAAACCCCTCTCAGTTGGATTGACGCTGCACTGCCTGTGATGAGCC	217
Q	y	1326	G	A	ATGCTAGTAATCGCGGATCAG-AATGCCCGGTGAATAGTTTCCCGGGCTTTGAC	1384
D	b	216	G	E	AACTGCTAGTAATCGCGGCTCAGCCATACGCGGTTGAATTCGTTCCCGGGCTTTGAC	157
Q	y	1385	A	C	ACCGCGCTCACACCAATGGAGTTCATGCAACAGAGTGGTTAGCTTAA-CTTAGTG	1443
D	b	156	A	C	ACCGCGCTCACACTATGGAGCTGGCCATGGCCGAAGTCGTTACCTTAAACCGCAAG	97
Q	y	1444	A	G	GCGCATCACACCGTGTGTGATGACTTGGGTGAAGTCGTAPCAAAAGTAGCGGTAGG	1503
D	b	96	A	G	GSGGTGCCAAGGCAAGGCTAGTGACTTGGNGTGAAGTCTGTAACAGGTAGCGTACT	37
Q	y	1504	G	A	AACTGCGGCTGGATCAC	1523
D	b	36	G	E	AAAGTGGCGCTGGAACCC	17

RESULT 4	BZ463550/c	BZ463550	1044 bp	DNA	linear	GSS 13-DEC-2002
LOCUS						
DEFINITION		BONKC86TF BO_1.6_2_KB_tot				Brassica oleracea genomic clone BONKC86,
						genomic survey sequence.
ACCESSION		BZ463550				

VERSION BZ463550.1 GI:26749465  
 KEYWORDS GSS.  
 SOURCE Brassica oleracea  
 ORGANISM Brassica oleracea  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 ; eurosids II; Brassicales; Brassicaceae; Brassica.  
 REFERENCE 1 (bases 1 to 1044)  
 AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.  
 TITLE Whole genome shotgun sequencing of Brassica oleracea  
 JOURNAL Unpublished  
 COMMENT Other\_GSSs: BONK86TR  
 Contact: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TF  
 Class: sheared ends.  
 Location/Qualifiers  
 1..1044  
 /organism="Brassica oleracea"  
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 /db\_xref="taxon:3712"  
 /clone="BONK86"  
 /clone\_lib="BO.1.6.2\_KB\_tot"  
 /notes="Vector: pHOS1; Site 1: 1.6-2 kb sheared  
 total DNA inserted into pHOS1 using BstXI linkers"  
 BASE COUNT 199 a 327 c 261 g 257 t  
 ORIGIN  
 Query Match 39.8%; Score 606.8; DB 29; Length 1044;  
 Best Local Similarity 78.4%; Pred. No. 7.8e-158;  
 Matches 764; Conservative 0; Mismatches 207; Indels 3; Gaps 3;  
 QY 466 CGATGACATTAGTCGCAGTAATACACCGCGTAACCTCTGTCGACGACGCGCGGTAATAC 525  
 Db 1002 CAATGACGGTATCTGGGAATATAGCATCGGCTAATCTGTGTCGACGACGCGCGGTAATAC 943  
 QY 526 AGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGACGAGCGTAGGTGGCTTGATAA 585  
 Db 942 AGAGGATGCAAGCGTTATCCGGATGATTGGCGTAAAGCGTCTGTAGGTGGCTTTTAA 883  
 QY 586 CTCAGATGTAAATCCCGGGCTTAACCTGGGACTGCACTGAACTGTGAACTGTAGGCTAGAG 645  
 Db 882 GTCCGCGCTCAATCCAGAGGCTCAACCCGTGACAGCGGTGGAACCTACACAGCTTTAG 823  
 QY 646 TAGGTGAGAGGGAAGTAGAATTCAGGTGTAGCGGTGAATTCGTAGAGATCTGAAGAA 705  
 Db 822 TACGGTAGGGCAGAGGAATTCGGTGTGAGCGGTGAATTCGTAGAGATCGAAGAA 763  
 QY 706 TACCGATGCGAGGACAGCTCTCTGGCATCATPACTGACACTGAGGCTCGAAGACGTGGGT 765  
 Db 762 CACCAAGCGGAAAGCACTCTGTGGCGCACACTGACACTGAGACAGCAAGAGCTAGGGG 703  
 QY 766 ASCAAACAGGATTAGATACCTTGTTAGTCACGCGCGTAAACGATGTCTACTAGTCGTTGG 825  
 Db 702 AGCGAATGGGATTAGATACCCAGTACTCTAGCCGTAAACGATGGATCTAGGCGCTGT 643  
 QY 826 GTCCCTTAGGACT-TAGTGACGAGCTAATAGCATATAGTAGACCGCTGGGGAGTACGG 884  
 Db 642 CGGTATCGACCGCTGCAGTGTCTGTAGTACACGCTTAAGTATCCCGCTGGGGAGTAGGT 583  
 QY 885 CGCGAAGTTTAAACTCAATGAATTCAGCGGGGCCCCACAAAGCGTGGAGCANTGCGT 944  
 Db 582 TCGCAAGATGAATCTCAAGAGATTGACGGGGGCCCCACAAAGCGTGGAGCANTGCGT 523  
 QY 945 TTAATTCGATGCAAGCGGAAGACCTTACCTGGTCTTGACATACACAGATCTTTAGAG 1004  
 Db 522 TTAATTCGATGCAAGCGGAAGACCTTACCGAGGCTTCGATGCGCGCATCTCTTCAA 463



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RESULT 6
BZ447500/c
LOCUS
DEFINITION
  BZ447500
  1053 bp DNA linear GSS 13-DEC-2002
  BONK40TR BO.1.6.2_KB_tot Brassica oleracea genomic clone BONK40,
  genomic survey sequence.
ACCESSION
  BZ447500
VERSION
  BZ447500.1 GI:26712943
KEYWORDS
  GSS.
SOURCE
  Brassica oleracea
  ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
  ; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 1053)
  Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
  Whole genome shotgun sequencing of Brassica oleracea
  Unpublished
  Other_GSSs: BONK40TF
  Contact: Chris Town
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA.
  Tel: 301-838-3523
  Fax: 301-838-0208
  Email: ctown@tigr.org
  DNA is from a doubled haploid provided by Tom Osborn.
  Seq primer: TR
  Class: sheared ends.
  Location/Qualifiers
    1..1053
    /organism="Brassica oleracea"
    /mol_type="genomic DNA"
    /strain="TO100DH3"
    /db_xref="taxon:3712"
    /clone="BONK40"
    /clone_lib="BO.1.6.2_KB_tot"
    /note="vector: pHS1; Site.1: 1.6-2 kb sheared
    total DNA inserted into pHS1 using BstXI linkers"
  BASE COUNT
    200 a 338 c 248 g 267 t
  ORIGIN
    Query Match 39.8%; Score 606.6; DB 29; Length 1053;
    Best local similarity 76.4%; Pred. No. 8.9e-158;
    Matches 818; Conservative 0; Mismatches 225; Indels 27; Gaps 5;

  QY 228 GTCTGATTAGCTAGTGGTAAAGCGCTACCATGGCGAGATCTGTAGCTGGTCTG 287
  DB 1045 GTCTGATTAGCTAGTGGTAAAGCGCTACCATGGCGAGTATGATGATGCTGGTCCG 986

  QY 288 AGAGGATGATCAGCCACACCGGACTGAGACACGCGCCGACT-CTACGGAGGACGACG 346
  DB 985 AGAGGATGATCAGCCACACCGGACTGAGACACGCGCCGACTCTCTACGGAGGACGACG 926

  QY 347 TGGGAATATGGCAATGGGAAACCTGATCCAGCATCGCGGTGTGGAAGAAGG 406
  DB 925 TGGGAAT-ATCCGCAATGGGCAAGACCTGACGAGCAATGCGGTGTGGAAGAAGG 867

  QY 407 CCTTTGGTTTAAAGCACTTTAAGCACTGAAGAGACTCTTCGGTTAATACCGGGGAC 466
  DB 866 CTTACGGTTCCTGAACTCTTTCCAGAGAAGAG-----C 830

  QY 467 GATGACATAGCTGCAATAAGACCGGCTACTCTGTGCGAGCAGCGCGGTAAATACA 526
  DB 829 AATGAGGGTATCTGGGAATAAGCATCGGCTAACTCTGTGCGAGCAGCGCGGTAAATACA 770

  QY 527 GAGGTGCAAGCGTTAATCGGAATTAATGCGGTAAAGCGAGTGGTCTGATTAAG 586
  DB 769 GAGGTGCAAGCGTTAATCGGAATTAATGCGGTAAAGCGTGGTCTGATTTAAG 710

  QY 587 TCAGATGTGAATCCCGGGCTTAACCTGGGAACCTGATCTGAAACTGTAGCTAGT 646
  DB 709 TCGCGCGTCAATCCCGGGCTCAACCTGGGACAGCGGTGGAACACTACCAAGCTTGA 650

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QY 647 AGGTGAGAGGGAAGTAGAATTCAGGTGTAGCGGTGAATTCGCTAGAGATCTGAGAGGAT 706
DB 649 ACCTGAGAGGCGAGGGAATTCGCGTGTAGCGGTGAATTCGCTAGAGATCTGAGAGGAAAC 590
QY 707 ACCGATGGCGAGGACGCTTCCTGGGCATCATCTGACACTGAGGCTCGAAAGCGTGGGTA 766
DB 589 ACCACGCGGAAAGCATCTCTGCTGGGCCACACTGACACTGAGAGCAGAAAGCTAGGGA 530
QY 767 GCAACAGGATTAGATACCTCTGCTAGTCCACCGCCGTAAGATGTCTACTAGTCTGGG 826
DB 529 GCAATGGGATTAGATACCTCTGCTAGTCCACCGCCGTAAGATGTCTACTAGTCTGGG 470
QY 827 TCCTTTGAGGACTT-AGTGAGCGAGCTAAGCAATAAGTACGCGCTGGGGAGTACGGC 885
DB 469 CGTATCGACCGCTGAGTGTGTAGCTAAGCGTTAAGTATCCCGCTGGGAGTACGTT 410
QY 886 CGCAAGGTTAAACTCAAAATTAATGACGCGGGCCGCCACAGCGGTGGAGCATGTGGTT 945
DB 409 CGCAAGATGAAGTCAAAAGGAATTGACGCGGGCCGCCACAGCGGTGGAGCATGTGGTT 350
QY 946 TAATTCGATGCAACGCGAGAACCTTACCTGGTCTGTGATACACACAGAACTCTGTAGAGA 1005
DB 349 TAATTCGATGCAACGCGAGAACCTTACCGAGGCTGTGATCCCGGAAATCTCTTTGAAA 290
QY 1006 TAGCAGAGTCCCTTCGGGAATTTGATACAGGTGTGATGCTGCTGCTGCTGCTGCTGTC 1065
DB 289 GAGAGGGGTGCCTTCGGGACGCGGACAGAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCC 230
QY 1066 GTGAGATGTGGTTAAGTCCCGACAGCGACACCTTCTCTTACTAGTACCAACATTT 1125
DB 229 GTAAGGTGTGGTTAAGTCCCGACAGCGACACCTTCTCTTACTAGTACCAACATTT 171
QY 1126 CGGTGGGAACTCTAAGGATACTGCCAGTACACAACTGGAGAGGCGGGGACGAGTCA 1185
DB 170 GAGTTTGGAACTCTAAGGATACTGCCAGTACACAACTGGAGAGGCGGGGACGAGTCA 111
QY 1186 AGTCATCAGGCGCTTACGACAGGCTGATACAGCTGTGATGCTGTGATGCTGTGATGCTGTG 1245
DB 110 AGTCATCAGGCGCTTACGACAGGCTGATACAGCTGTGATGCTGTGATGCTGTGATGCTGTG 51
QY 1246 AGCTACACAGCGATGTGATGCGAATCTCAAAAGCGCTATCGTAGTCCAGA 1295
DB 50 CGCGATCGAGAGGGGTGAGTAACTCCAAAACCGCTCTCAGTTGGA 1

RESULT 7
BZ431523/c
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DEFINITION
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  1010 bp DNA linear GSS 13-DEC-2002
  BONHD88TF BO.1.6.2_KB_tot Brassica oleracea genomic clone BONHD88,
  genomic survey sequence.
ACCESSION
  BZ431523
VERSION
  BZ431523.1 GI:26677909
KEYWORDS
  GSS.
SOURCE
  Brassica oleracea
  ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
  ; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 1010)
  Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
  Whole genome shotgun sequencing of Brassica oleracea
  Unpublished
  Other_GSSs: BONHD88TF
  Contact: Chris Town
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA.
  Tel: 301-838-3523
  Fax: 301-838-0208
  Email: ctown@tigr.org
  DNA is from a doubled haploid provided by Tom Osborn.
  Seq primer: TF
  Class: sheared ends.
  Location/Qualifiers

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/strain="T0100DH3"
/db_xref="taxon:3712"
/clone="BONHD88"
/clone_lib="BO.1.6.2_KB.tot"
/notes="Vector: pHS1; Site_1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHS1 using BstXI linkers"
BASE COUNT 192 a 327 c 236 g 255 t
ORIGIN
Query Match 39.68; Score 603.6; DB 29; Length 1010;
Best Local Similarity 77.13; Pred. No. 6e-157;
Matches 795; Conservative 0; Mismatches 210; Indels 26; Gaps 4;
QY 232 GATTAGCTAGATGGTGGGTAAGAGCCATCATGGCGAGCATCTGTAGCTGTCTGAGAG 291
DB 1010 GATTAGCTAGTGGTGAGGCATAGCTTACCAGGCGATGATCAGTAGCTGTCTGAGAG 951
QY 292 GATGATACGCCACACCGGAGCTGAGACACGCCGCCGGACT-CTACGGGAGGCGACAGTGGG 350
DB 950 GATGATCAGCACACTGGGACTGAGACACGCCGCCGGACTCTTACGGGAGGCGACAGTGGG 891
QY 351 GAATATGGCAATGGNGSAACCTGTATCCAGCCATGCGCGTGTGTGAAGAGGCTT 410
DB 890 GAATTTCCGATGGCGAAGAGCCTGACGGAGCAATCCCGCTGGAGTAGAGGCGTA 831
QY 411 TTGGTTGTAAGACACTTAAGCAGTCAAGAAGACTCTTGGTTTAATACCCGGGACGATG 470
DB 830 CGGGTCTGAACITCTTCCAGAGAGAG-----CAATG 794
QY 471 ACATTAGCTGAGATAAGCACCGGCTAATCTGTGCGACACGCCCGGTAAATACAGAGG 530
DB 793 ACAGTATCGGGGATAAGCATCGGCTAATCTGTGCGACAGCCCGCGGTAATACAGAGG 734
QY 531 GTGCAAGCGTTAATCGGTAATCTGGCGTAAAGCGAGCTAGTGGCTGTGATAGTCAG 590
DB 733 ATGCANGCGTTATCCGGAATGATGGCGGTAAAGCGTCTGTAGGTGGCTTTTAAGTCGG 674
QY 591 ATGTGAATCCCGGGCTTAACCTGGGAACCTGCATCTGAACCTGTWAGGCTAGAGTGGT 650
DB 673 CGGTCAATCCAGGGCTCAACCTGGACAGCGGTGGAACCTACCAAGCTTGATGACGG 614
QY 651 GAGAGGAGTAGTAATTCAGGTGTAGCGGTAAATCCGTAGAGATCTGAAGAGTAACCG 710
DB 613 TAGGGCAGAGGGAATTCGGGTGGAGCGGTGAATCGTAGAGATCGGGAAGAACACCA 554
QY 711 ATGGCGAGGAGCTCTCTGGCATCATACTGACACTGAGGCTCGAAGCGTGGGTAGCAA 770
DB 553 ACGGGAAGAGCACTCTGCTGGGCGCACACTGACACTGAGAGACGAAGCTAGGGAGCGA 494
QY 771 ACAGGATTAGATACCTCTGTAGTCTCCACCGCTAAACAGTGTCTACTAGTTCGTTGGTCC 830
DB 493 ATGGGATTAGATACCCCACTAGTCTAGCCGTAAACAGTGTAGTACGCTGTGGCTA 434
QY 831 TTGAGGACT-TAGTACGAGCTAGTACGCAATAGTACGCCCTGGGAGTAGCGCCGCA 889
DB 433 TCGAACCCGCTGCTGTAGTCTAACGGTTAAGTATCCCGCTGGGAGTAGTTCGCA 374
QY 890 AGGTTAAACTCAAAATGAATTGACGGGGCCCGCACAGCGGTGGAGCATGTGGTTTAA 949
DB 373 AGAATGAACATCAAGGAATGACGGGGCCCGCACAGCGGTGGAGCATGTGGTTTAA 314
QY 950 TCGATGCAACCGAAGAACCTTACCTGTCTTGATACACAGAAATCTTGTAGAGATACG 1009
DB 313 TCGATGCAAGCAAGAACCTTACCGAGGCTTGATACCGCCGCAATCTTGTGAAGAGA 254
QY 1010 AGAGTGCCTTCGGGAATTTGTGATACAGTGTGATGGCTGTGCTGAGTGTGCTGTG 1069
DB 253 GGGGTGCTTCGGGAACCGGAGACAGAGTGTGATGGCTGTGCTGAGTGTGCTGCTG 194
QY 1070 GATGTGGGTAGTCCCGCACAGGAGCGCAACCTTGTCTTGTAGTTACAGCACTTCGGG 1129
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Db 193 GGTGTGGGTAAAGTCCCGCAACGAGCGCAACCTTCGTGTTAGTTGCCA-CGGTTAGT 135
QY 1130 TGGGAACCTCTAAGGATACCTCCAGTGCACAACTGAGGAGGCGGAGCAGCAAGTCAAGTC 1189
DB 134 TTGGAAACCTGAACAGACTCCCGGTGATGAAGCCGGAGGAGGTGAGGATGACGTCAAGTC 75
QY 1190 ATCATGGCCCTTAGCAGCAGGCTACACACGCTGTACACAGTGTGTAGGTAGTACAGAGGCAAGCT 1249
DB 74 ATCATGGCCCTTAGTCCCTGGCGACACACGCTGTGTACAAATGGCGCGGACAAAGGTCGCG 15
QY 1250 ACACAGCGCATG 1260
DB 14 ATCCGCGGAGG 4
RESULT 8
BH656222/c
LOCUS BH656222 1031 bp DNA linear GSS 19-FEB-2002
DEFINITION BOMJ286TF BO_2_3_KB Brassica oleracea genomic clone BOMJ286,
genomic survey sequence.
ACCESSION BH656222
VERSION BH656222.1 GI:18714532
KEYWORDS GSS
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
REFERENCE 1 (bases 1 to 1031)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished
COMMENT Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: Tg
Class: Sheared ends.
FEATURES
Location/Qualifiers
source 1. .1031
/organism="Brassica oleracea"
/mol_type="genomic DNA"
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/db_xref="taxon:3712"
/clone="BOMJ286"
/clone_lib="BO_2_3_KB"
/notes="Vector: pHS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHS1 using BstXI linkers"
BASE COUNT 198 a 327 c 250 g 256 t
ORIGIN
Query Match 39.58; Score 602.6; DB 28; Length 1031;
Best Local Similarity 75.74; Pred. No. 1.2e-156;
Matches 795; Conservative 0; Mismatches 230; Indels 25; Gaps 3;
QY 331 CTACGGGAGGAGCAGTGGGGAATATGGACAATGGNGGGAACCTGTATCCAGCATGCC 390
DB 1027 CTACGGGAGGAGCAGTGGGGAATTTCCGCAATGGGGAAGCCCTGACGGCAATGCC 968
QY 391 GCGTGTGTGAAGAGGCGCTTTGGTTGTAAAGACACTTTAAGCAGTGAAGAAGACTCTTCG 450
DB 967 GCGTGGAGTAGAGGCTTACGGGCTCTCACTCTTTTCCAGAGAGAAG-----916
QY 451 GTTAATATCCCGGAGCATGACATAGTGTGAGTAAGCAACCGGTAACTCTGTGCGAG 510
DB 915 -----CAATGACGGTATCTGGGGAATAGCATCGGCTAACTCTGTGCGAG 871
QY 511 CAGCCGCGGTAAATACAGAGGCTGACAGGTTAATCGGAATTAAGTGGCGTAAAGCGAGCG 570
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870	Db	CAGCCCGGTAATACAGAGGATCGAAGCGTTATCCGGAAATGATTGGCGGTAAAGCGTCTG	811
571	QY	TAGTGGCTTGATTAAGTCAGATGTGAATCCCGGGCTTAACCTGGGAACTGCATCTCAA	630
810	Db	TAGTGGCTTTTAAAGTCCGCGGTCAAAATCCCAAGGGCTCAACCCCTGGACAGCGGTGCAA	751
631	QY	ACTGTTAGCTAGACTAGGTGAGAGGAAAGTAGAATTCACAGTCTAGCGGTGAATGCGT	690
750	Db	ACTACCAAGCTTGATACGTTAGGGGACAGAGGAATTTCCGGTGGAGCGGTGAATGCGT	691
691	QY	AGAGATCTGAAGGAATACCGATGGCGAAGCAGCTCTCTGGCATCATATGTCACACTGAGG	750
690	Db	AGAGATCGGAAAGAACCAACGCGCAAGACACTCTGCTGGGCGCACACTGACACTGAGA	631
751	QY	CTCGAAGCGTGGGTAGCAACACAGGATAGATACCCCTGGTAGTCCACGCGCTAAACGATG	810
630	Db	GAGCAAGCTTAGGGAGCGAATGGGAATAGATACCCCAAGTAGTCTTAGCCGCTAAACGATG	571
811	QY	TTACTAGTCTGTTGGTCCCTTGAGGACT-TAGTCACGACGCTAAACGCAATAGTAGAC	869
570	Db	GATACTAGGGCTGTGGCTATCGACCCGTGCAGTCTGTACTAACCGGTTAAGTATCCC	511
870	QY	GCTGGGGAGTACGGCCGCCAAGGTTAAACTCAATGAATTAACGGGGGCCGCAACG	929
510	Db	GCTTGGGAGTAGCTTCCCAAGAAATGAATCAAAAGGAATTAACGGGGGCCGCAACG	451
930	QY	GGTGGAGCATGTTTAATTCGATCGACGCGGAGACCTTACCTGGTCTTGACATACA	989
450	Db	GGTGGAGCATGTTGTTTAATTCGATCGAAGCGAAGACCTTACAGGGCTTGACATGCC	391
990	QY	CAGAACTTGTAGAGATACGAGATGCTTCGGGAATTTGTATACAGGTCTGCATGCT	1049
390	Db	CGGAATCCTCTTGAAGAGAGGGTGCTTCGSGAACCGCACACAGGTGGTGCATGCC	331
1050	QY	GTGCTCAGCTCTGCTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTTGTC	1109
330	Db	GTGCTCAGCTCTGCTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTTGTC	271
1110	QY	TTAGTTACCAGCACTTCGGGTGGAACTCTAAGGATACTGCCAGTGACAACTGGAGAA	1169
270	Db	TTAGTTGCCA-CGGTTGAGTTTGAACCTTGACAGACTGCCGTTGATANGCGGAGAA	212
1170	QY	GGCGGGACAGCTCAAGTATCATATGCGCCCTTACGACCAGGGCTPACACAGTGTCTACAA	1229
211	Db	GGTGAAGATCAAGTCAAGTATCATATGCGCCCTTAAGCCCTGGGCGACACAGTGTACA	152
1230	QY	GGTAGTACAGAGGCGCACTPACACAGGATGTGATGCGAATCTCAAAAGCCCTATCGTAG	1289
151	Db	GGCGGGACAAAGGTCGCGATCCCGGGAGGTGAGCTPACTCCAAHAACCCGCTCTCAG	92
1290	QY	TCCAGATTTGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGATCA	1349
91	Db	TTGCGATTGCGAGCTGCAACTCGCTTCATGAAGCGGAATCGATAGTAATCGCGGTCA	32
1350	QY	GAATCGCGGTGAATAGTTCCCGGGCCW	1379
31	Db	GCCATACGCGCGGAATTCGTTCCCGGGCCT	2

RESULT 9	
BZ450751	
LOCUS	1077 bp DNA linear GSS 13-DEC-2002
DEFINITION	BONQ63FR BO.1.6_2_KB_tot Brassica oleracea genomic clone BONB063, genomic survey sequence.
ACCESSION	BZ450751
VERSION	BZ450751.1 GI:26721334
KEYWORDS	GSS.
SOURCE	Brassica oleracea
ORGANISM	Brassica oleracea
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids I; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 1077)



QY	1125	TCGGTGGGAACCTAAGGATATCGCACTGACAAACTGGAGGAAAGCGGGGACGACGTC	1184
Db	725	TGAGTTTGAAACCCCTGACACACTGCCGTGTATAGCCGGAGGAAGGTGAGGATGACGTC	784
QY	1185	AAGTCATCATGCGCCCTTACGACACAGGGCTACACAGCTCTACATATGTTAGGTACAGAGG	1244
Db	785	AAGTCATCATGCGCCCTTATGCCCTGGCGACACAGTCTACATATGCCGGGACAAAGG	844
QY	1245	CAGCTACACAGCGATGTGATCGGAACTCTAAAGACCTATCTAGTCCAGATGGAGTCT	1304
Db	845	TCGCGATTCGGCGAGGGTGAAGCTAACTCCAAAGACCGTCTCAGTTCGAGATTGAGGCT	904
QY	1305	GCAACTCGACTCCATCAAGTAGTAGGAATCGCTAGTAAATCGCGATCAG -AATGCGCGGGTGA	1363
Db	905	GCAACTCGCTGCATGAAGCGGAATCGCTAGTAAATCGCGGTCGCCCATCGGCGGTGA	964
QY	1364	ATAGCTTCGGGGCCCTTGCTACACACCGCCGGTACACACATGGGAGGTGTGATTGCAACGAA	1423
Db	965	ATTGCTTCGGGGCCCTTGCTACACACCGCCGGTACACACTATGGGAGTGGCCATGCCCGAA	1024
QY	1424	GTGGTTAGCGCTAAC	1437
Db	1025	AGTCGTACCTTAAC	1038

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RESULT 10          BZ426201/c
LOCUS              BZ426201        1016 bp      DNA       linear    GSS 13-DEC-2002
DEFINITION         BONDZ28TF BO_1.6_2_KB_tot Brassica oleracea genomic clone BONDZ28,
                    genomic survey sequence.
ACCESSION           BZ426201
VERSION             BZ426201.1   GI:26667713
KEYWORDS            GSS.
SOURCE              Brassica oleracea
ORGANISM            Brassica oleracea
REFERENCE            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                     Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
                     II; Brassicales; Brassicaceae; Brassica.
AUTHORS             Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE               Whole genome shotgun sequencing of Brassica oleracea
JOURNAL             Unpublished
COMMENT             Other_GSs: BONDZ28TR
                   Contact: Chris Town
                   TIGR
                   9712 Medical Center Drive, Rockville, MD 20850, USA.
                   Tel: 301-838-3523
                   Fax: 301-838-0208
                   Email: cdtown@tigr.org
                   DNA is from a doubled haploid provided by Tom Osborn.

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	Query Match	39.0%;	Score 595.2;	DB 29;	Length 1016;
	Best Local Similarity	77.2%;	Pred. No. 1.3e-154;		
	Matches 797;	Conservative	0;	Mismatches 209;	Indels 27; Gaps 5;
QY	228	GTGCGATTACGCTAGATGTTGGGTAAAGCCCTACCACTGGCGAGCATCTCTAGCTGGTCTG	287		
DB	1008	GTCGTATTACGCTAGTGGTGAGGCAATAGCTTACCAGGGGAGTATCATCTAGCTGGTCCG	949		

QY	288	AGAGGATGATCAGCCACACCGGGACTGAGACACGCGCCCGGACT-CTACGGGAGGCGACGAG	344
Db	948	AGAGGATGATCAGCCACACCGGGACTGAGACACGCGCCCGGACTCTCTACGGGAGGCGACGAG	889
QY	347	TGGGGAAATTTGGACAAATGGNGGAAACCTTGATTCAGCCATCCGCGGTGTGTGAAGAAG	406
Db	888	TGGGGAAAT-TTCGCAATGGCGAAAGCCCTGACGAGCAATGCCGCGTGGAGGTAGAAG	830
QY	407	CTTTTGGTTTGAAGACACTTTTAAGCAGTGAAGAAGACTCTTCGGTTTAATACCCGGGGAC	466
Db	829	CTCAGGGTCTCGAATCTCTTTCCCAAGAAAGAG-----C	793
QY	467	GATGACATTTAGTTCGCAAGTAAGACACCGGTACTCTGTGCACAGACCGCGGTAAATCA	526
Db	792	AATGACGGTATCTGGGAATAGCATCGGCTAACTCTGTGCACAGACCGCGGTAAATCA	733
QY	527	GAGGTCTAGCGTTAATCGGGAATTAAGTCTGGGCGTAAAGCGAGCGTGGTGGCTGTATAG	586
Db	732	GAGGATCAGACGGTTATTCGGAATGATTTGGCGTAAAGCGTCTGTAGGTGGCTTTTATAG	673
QY	587	TCAGATGTAAATCCCGGGGCTTAACCTGGGAACCTGCATCTGAAACTGTTAGGCTAGAGT	646
Db	672	TCCCGCTCAATCCCGGGGCTCAACCTGGACAGCGGTGGAACACTACCAAGCTTGAGT	613
QY	647	AGGTTCAGAGGGAAGTAGAATTCAGGTGTAGCGGTGAATCCGTAGAGATCTGAAGGAAT	706
Db	612	ACGTTAGGGCAGAGGGAATTTCCGGTGGAGCGGTGAATCGTAGAGATCGGAAGAAGAC	553
QY	707	ACCGATGGCAGAGGAGTTCCTGGCATCATCTGACACTGAGGCTCGAAAGCGTGGGTA	766
Db	552	ACCAACGGCGAAGCACCTCTCTGGCGCGACACTGCACCTGAGAGACGAAGCTAGGGGA	493
QY	767	GCAACAGAGTTAGATACCTTGGTAGTCCACGCGGTAAACGATGCTACTAGTCTGTGGG	826
Db	492	CGGAATGGGATTAGATACCCAGTAGTCTAGCCGTTAACGATGATGATGATGAGCGCTGTG	433
QY	827	TCCTCTGAGGACT-PAAGTCAGCAGCTAACCGCAATAGTACGCGCTGGGGAGTAGCGG	885
Db	432	CGTATACGCCCTGCGAGTGTGTAGCTAACCGCTTAAGTATCCCGCTGGGGAGTAGCTT	373
QY	886	CGCAAGGTTAAACTCAATGAAATTGACGGGGGCCCGCACAGCGGTGGAGCATGTGGTT	945
Db	372	CGCAAGAATCAAACTCAAAGGAATTGACGGGGGCCCGCACAGCGGTGGAGCATGTGGTT	313
QY	946	TAAATCATGACCAACGCGAAGAACCTTACTGTGCTTTGACATACACAGAACTTTGTATAGA	1009
Db	312	TAAATCATGACCAAGCGAAGAACCTTACCAGGCGTTGACATGCCGGAATCCCTTTGAAA	253
QY	1006	TACGAGAGTGCCTTCGGGAATTGTATACAGGTGCTTGCATGCGTCTGCTCAGCTCGCTGC	1065
Db	252	GAGAGGGTGCCTTCGGGAACGCGACACAGGTGGTGTGATGSGTGTGCTCAGCTCGTGC	193
QY	1066	GTGAGATGTGGTTAAGTCCCGCAACGAGCGCAACCCCTTGTCTTATGTTACACAGCACTT	1129
Db	192	GTAAGTGTGTGGTTAAGTCCCGCAACGAGCGCAACCCCTTGTGTATGTTGCA-CCGTT	134
QY	1126	CGGTGGGAACCTCTAAGGATACTCCCAAGTGACAAACTGGAGGAAGCGGGAGCAGCTCA	1183
Db	133	GAGTTTGGAAACCTGACACAGACTCCCGGTGTATAGCCGGAGGAAGGTGTAGGATGACCTCA	74
QY	1186	AGTCATCATGGCCCTTACGACCCAGGGCTACACACGTTGCTTACAAATGGTAGGTACAGAGGC	1245
Db	73	AGTCATCATGGCCCTTATGTCCTGGGCGACACAGCTACTACAAATGCCCGGACAAAGGTT	14
QY	1246	AGCTACACAGCA	1258
Db	13	CGCGATCCCGCA	1

RESULT 11  
BH705272  
LOCUS

BH705272	1079 bp	DNA	linear	GSS 20-FEB-2002
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BASE COUNT 159 a 230 c 164 g 187 t 1 others
ORIGIN
Query Match 38.28; Score 582.4; DB 14; Length 741;
Best Local Similarity 87.44; Pred. No. 4.1e-151;
Matches 648; Conservative 0; Mismatches 92; Indels 1; Gaps 1;
374 CCTGATCCAGCATCGCCGCTGTGTAAGAAGGCTTTTGGTTGTAAGCACTTTAAGCA 433
Db 740 CTTGATCCAGCATCGCCGCTGTGTAAGAAGGCTTTTGGTTGTAAGCACTTTAAG-T 682
Qy 434 GTGAAGAAGACTCTTCGGTTTAATACCGGGGAGCATGACATAGCTGCAGAAATAAGCACC 493
Db 681 GGGAGGAAGGCTTTACAGCAATACCTCTGTAGTTTTCAGCTTACCGACAGAAATAGCACC 622
Qy 494 GGCTAACTCTGTCAGCAGCGCGGTATACAGAGGGTCAAGCGTTAATCGGAATTAC 553
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Qy 734 TCATACCTGACACTGAGCTCGAAGCGTGGGTAGCAACAGAGATTAGATACCTCGTAGT 793
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Qy 854 AGCCTAATAGTAGACCCCTCGGGAGTAGCGCCGAGGTAAACCTCAATGAATTGAC 913
Db 261 AGCCTAATAGTAGACCCCTCGGGAGTAGCGCCGAGGTAAACCTCAATGAATTGAC 202
Qy 914 GGGGCCCGCACAAGCGGTGGAGCAATGTGTTAATTCGATCAACGCGGAAGAACTTAC 973
Db 201 GGGGCCCGCACAAGCGGTGGAGCAATGTGTTAATTCGATCAACGCGGAAGAACTTAC 142
Qy 974 CTGGTCTTGACATACAGAACTCTGTAGAGTACGAGAGTGCTTCGGGAATTTGATA 1033
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RESULT 13  
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LOCUS BH814966 1143 bp DNA linear GSS 31-MAY-2003
DEFINITION BBPCL5 Maize B chromosome PCR DNA library Zea mays genomic clone
ACCESSION BH814966
VERSION BH814966.1 GI:31249923
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1143)
AUTHORS Cheng, Y. M. and Lin, B. Y.
TITLE Cloning and characterization of maize B chromosome sequences
derived from microdissection
JOURNAL Genetics 164 (1), 299-310 (2003)
MEDLINE 22635479
PUBMED 12750341
COMMENT Contact: Bor-yaw Lin
Department of Molecular Biology
National Chung Hsing University
250 Kuo Kuang Rd, Taichung 402, Taiwan (ROC)
Tel: 886-4-2285-1885
Fax: 886-4-2287-4879
Email: bylin@dragon.nchu.edu.tw
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/cell_type="Pollen mother cells"
/dev_stage="Meiosis I"
/lab_host="DH5alpha"
/clone_lib="Maize B chromosome PCR DNA library"
/notes="Vector: pBSK-; The library was constructed from
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Query Match 37.58; Score 571.6; DB 28; Length 1143;
Best Local Similarity 82.84; Pred. No. 5.3e-148;
Matches 727; Conservative 0; Mismatches 139; Indels 12; Gaps 6;
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Qy 892 GTTAAACTCAAAATGAATTGACGGGGGCGCCGACAAAGCGGTGGAGCATGTGGTTAAATTC 951
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Db 843 GATGCAACGCGAAGAACCTTACCTGGTCTTGACATACACAGAACTCTGTAGAGTACGAG 784
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QY      1250  ACACAGGATGATGCGGAATCTCAAAAAGCCTATCGTAGTCCAGANTGGAGTGCACAC 1309
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QY      1310  TCGACTCCATGAGTAGGATCGTAGTATCCGATCAGATACGATCCCGGTGAATACGT 1369
Db      491  TCGACTGATGAGTGTGATGTAGTATTCGCGATCAGATGCGCGGTGAATACGT 432
QY      1370  TCCCGGCGCTTATACACACCGCCGCTCACACCTAGTGGAGTTCGATGACACAGAGTGT 1429
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QY      1430  ASCTAA-CTTAGTAGGCGATCACACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1488
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DEFINITION BOKN51tr BO.1.6.2_KB lot Brassica oleracea genomic clone BOKN51, genomic survey sequence.
ACCESSION BZ440868
VERSION   BZ440868.1 GI:26698161
KEYWORDS  GSS.
SOURCE    Brassica oleracea
ORGANISM  Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 974)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished
Other_GSSs: BOKN51TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
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Best Local Similarity 77.3%; Pred. No. 7.1e-148;
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QY      737  TACTGACACTGAGGCTCGAAAGCGTGGTAGCAAAACAGGATTTAGATACCTGGTAGTCA 796
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QY      797  CGCGTAAAGCAGTGTCTACTAGTGTGGTTCCTTTAGGACT-TAGTGAAGCAGCTAAC 855
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QY      916  GGGCCGCAAGCGGTGGAGCATGTGTTAATTCGATGCAAGCGGAGGAGTGTACCT 975
Db      654  GGGCCGCAAGCGGTGGAGCATGTGTTAATTCGATGCAAGCGGAGGAGTGTACCT 713
QY      976  GGTCTTGACATACAGAGAACTTTGTAGATACAGAGTGCCTTCGGGAATTTGTATACA 1035
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ACCESSION  
VERSION  
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids II; Brassicales; Brassicaceae; Brassica.  
REFERENCE  
1 (bases 1 to 951)  
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.  
Whole genome shotgun sequencing of Brassica oleracea  
Unpublished  
Contact: Chris Town  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: TR  
Class: sheared ends.  
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GenCore version 5.1.6  
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Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

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- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

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#### SUMMARIES

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5	1098.6	72.0	1501	4	US-09-748-205-1
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11	1019.8	66.8	1540	4	US-09-228-184-1
12	1019.8	66.8	1540	4	US-09-967-376-1
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15	1008.8	66.1	1830121	4	US-09-643-990A-1
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18	983.2	64.4	1449	4	US-09-602-417-1
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20	931.8	61.1	1536	2	US-08-642-229A-1
21	927.8	60.8	1536	1	US-08-114-695A-7
22	922.6	60.5	1451	3	US-09-342-579-1
23	922.6	60.5	1451	4	US-09-617-854A-1
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#### ALIGNMENTS

RESULT 1  
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; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi  
; APPLICANT: Van Heuverswyn, Hugo  
; TITLE OF INVENTION: HYBRIDIZATION PROBES FOR THE  
; TITLE OF INVENTION: DETECTION OF BRANHAMELLA CATARRHALIS STRAINS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 No. 5721097west Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/299,810A  
; FILING DATE: 01-SEP-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hillson, Randall A.  
; REGISTRATION NUMBER: 31,838  
; REFERENCE/DOCKET NUMBER: 8076.70-US-WO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1485 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: Branhamella catarrhalis  
; IMMEDIATE SOURCE:  
; CLONE: 16S rRNA Gene  
US-08-299-810A-27

Query Match 78.3%; Score 1195; DB 1; Length 1485;  
Best Local Similarity 90.6%; Pred. No. 0;  
Matches 1352; Conservative 0; Mismatches 128; Indels 12; Gaps 7;

Db	1072	TACACAGCACTGGGTCGGGAACTCTAAGGATACTCCAGTACAAACTGGAGAAAGGGCG	1131
Qy	1175	GGACGAGCTCAAGTCATCATGCGCCCTTACGACACAGGGGTACACACGTCGTCAACAATGGTAG	1234
Db	1132	GGACGAGCTCAAGTCATCATGCGCCCTTACGACACAGGGGTACACACGTCGTCAACAATGGTTG	1191
Qy	1235	GTACAGAGGGCAGCTACACACGAGTGTGATGCGAATCTCAAAAAGCCTATCGTATGTCAG	1294
Db	1192	GTACAAAAGGGTGTCTACACACGAGTGTGATGCTTAATCTCAAAAAGCCAAATCGTATGTCGG	1251
Qy	1295	ATTGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGATCAACAATG	1354
Db	1252	ATTGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGATCAGAATG	1311
Qy	1355	CCGCGGTGAATAGTGTCCGGGCGCTTGTACACACGCGCCGTCACACCATGGGAGTGTGATT	1414
Db	1312	CTGCGGTGAATAGTGTCCGGGCGCTTGTACACACGCGCCGTCACACCATGGGAGTGTGATC	1371
Qy	1415	GCACACAGAGTGTAGGCTTAAGTAGGCGCATCACACCGTGTGTCGATGACTGT	1474
Db	1372	TACACAGAGTGTAGGCTTAAGTAGGCGCATCACACCGTGGGTGATGACTGT	1430
Qy	1475	GGGTCAAGTCGTAAAGTAGCCGTAGGGAACCTGGGGTGGATCAACCTC	1526
Db	1431	GGGTGAAGTCGTAAAGTAGCCGTAGGGAACCTGGGGTGGATCAACCTC	1481

RESULT 2  
 US-09-793-920A-1  
 ; Sequence 1, Application US/09793920A  
 ; Patent No. 6479621  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Canon Inc.  
 ; TITLE OF INVENTION: Polyoxyalkanoate containing 3-hydroxythienylalkanoic  
 ; FILE OF INVENTION: monomer unit, and method for producing the same.  
 ; FILE REFERENCE: 4396021  
 ; CURRENT APPLICATION NUMBER: US/09/793,920A  
 ; CURRENT FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 1  
 ; SEQ ID NO 1  
 ; LENGTH: 1501  
 ; TYPE: DNA  
 ; ORGANISM: Pseudomonas jessenii 161 strain.  
 US-09-793-920A-1

Qy	30	GGCGCAGGCTTAACACATGCAAGTCAGCGGAAACGATGATGCTTATTTAGCGTTC	89
Db	9	GGCGCAGGCTTAACACATGCAAGTCAGCGG--ATGACGGGAGCTTGCTCTGAATTCA	66
Qy	90	GAGCGCGGACGGGTGAGTAACTACTAGGAATCTACCTAGTGTAGTGGGGATAGCTCGGG	149
Db	67	G---CGGCGGACGGGTGAGTAACTGCTAGGATCTGCTTGTGTAGTGGGGACACGCTCTC	123
Qy	150	GAACTCGAATTAATACCCCATAGCT--CTACGGGAAAGCAGGGGNTCAATTAGACCTTG	208
Db	124	GAAGGGACGCTAATACCCCATACGCTCTACGGGAAAGCAGGGGACCTTCGGGCGCTTG	183
Qy	209	CGCTATTAGTAGCCCTAGTCGGATAGCTAGATGGTGGGTAAAGCCCTACCAATGGCG	268
Db	184	CGCTATCAGATGAGCCTAGTTCGGATAGTGTGCTGAGGTAATGGCTCACCAAGGCG	243
Qy	269	AGGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGAGCTGAGACACGGGCCGA	328
Db	244	ACGATCCGTAAGTGGTCTGAGAGGATGATCAGTCACTGCACTGAGACACGCTCCAGA	303
Qy	329	CT-CTACGGGAGCAGCATGGGGAATTTGGCAATATGNGNGGAACCCCTGATCCAGCAT	387
Db	304	CTCTCTACGGGAGCAGCATGGGGAATTTGGCAATATGNGNGGAACCCCTGATCCAGCAT	363



QY 388 GCGCGTGTGTGAAGAGAGCGCTTTTGGTGTAAAGACCTTTAAGCAGTGAAGAGACACT 447  
Db 364 GCGCGTGTGTGAAGAGAGCGCTTTTGGTGTAAAGACCTTTAAGCAGTGAAGAGACACT 423  
QY 448 TCGGTTAATACCGGGGACGATGACATTAAGTTCGAGATAGACACCGGTAACTCTGTC 507  
Db 424 TAACCTAATAGTGTAGTGTGTTGACGTTACCGAGATTAAGCAGTGAAGAGACACT 483  
QY 508 CAGCAGCGCGGTAAATACAGAGGTGCAAGCGTTAATCGGAATTAAGTTCGAGTGAAGAG 567  
Db 484 CAGCAGCGCGGTAAATACAGAGGTGCAAGCGTTAATCGGAATTAAGTTCGAGTGAAGAG 543  
QY 568 GCGTGTGTGTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 627  
Db 544 GCGTGTGTGTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 603  
QY 628 GAACCTGT 687  
Db 604 ARACTGT 663  
QY 688 CGT 747  
Db 664 CGT 723  
QY 748 AGCTCGAAGCGT 807  
Db 724 AGCTCGAAGCGT 783  
QY 808 ATGTCTGT 867  
Db 784 ATGTCTGT 843  
QY 868 CCGCTGT 927  
Db 844 CCGCTGT 903  
QY 928 GCGGT 987  
Db 904 GCGGT 963  
QY 988 CAGCAATCTGT 1047  
Db 964 CAATGT 1023  
QY 1048 CTGTCTGT 1107  
Db 1024 CTGTCTGT 1083  
QY 1108 CTTGT 1166  
Db 1084 CTTGT 1143  
QY 1167 GAAGCGGGGACGCTCAAGTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1226  
Db 1144 GAAGCGGGGACGCTCAAGTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1203  
QY 1227 AATGT 1286  
Db 1204 AATGT 1263  
QY 1287 TAGTCCAGATGT 1346  
Db 1264 TAGTCCAGATGT 1323  
QY 1347 TCAGATGT 1406  
Db 1324 TCAGATGT 1383  
QY 1407 AGT 1465  
Db 1384 AGT 1443

QY 1466 CGATGACTGGGTGAAGTCTGATACAGGTAGCCGTAGGGGAACCTCGGCTGGATCAC 1523  
Db 1444 TCATGACTGGGTGAAGTCTGATACAGGTAGCCGTAGGGGAACCTCGGCTGGATCAC 1501  
RESULT 3  
US-09-821-016-5  
; Sequence 5, Application US/09821016  
; Patent No. 6485951  
; GENERAL INFORMATION:  
; APPLICANT: CANON INC.  
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enz.  
; FILE REFERENCE: 4051021  
; CURRENT APPLICATION NUMBER: US/09/821,016  
; CURRENT FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 5  
; LENGTH: 1501  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii P161 ; BP-7376  
; FEATURE:  
US-09-821-016-5  
Query Match 72.08; Score 1098.6; DB 4; Length 1501;  
Best Local Similarity 85.98; Pred. No. 0;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;  
QY 30 GCGCGAGCTTAACACATGCTAGTGGGAAACGATGATAGTGTGTGTGTGTGTGTGTGT 89  
Db 9 GCGCGAGCTTAACACATGCTAGTGGGAAACGATGATAGTGTGTGTGTGTGTGTGTGT 66  
QY 90 GAGCAGCGGAGCTGCTAGTGGGAAACGATGATAGTGTGTGTGTGTGTGTGTGTGTGT 149  
Db 67 G---CGGCGAGCTGCTAGTGGGAAACGATGATAGTGTGTGTGTGTGTGTGTGTGTGT 123  
QY 150 GAACTCGGAATTAACACATGCTAGTGGGAAACGATGATAGTGTGTGTGTGTGTGTGT 208  
Db 124 GAAAGGAGCTTAACACATGCTAGTGGGAAACGATGATAGTGTGTGTGTGTGTGTGTGT 183  
QY 209 CGT 268  
Db 184 CGT 243  
QY 269 ACATGT 328  
Db 244 ACATGT 303  
QY 329 CT-CTACGGGAGCGAGCTGCTAGTGGGAAACGATGATAGTGTGTGTGTGTGTGTGTGT 387  
Db 304 CTCTACGGGAGCGAGCTGCTAGTGGGAAACGATGATAGTGTGTGTGTGTGTGTGTGTGT 363  
QY 388 GCGCGT 447  
Db 364 GCGCGT 423  
QY 448 TCGGTTAATACCGGGGACGATGACATTAAGTTCGAGATAGACACCGGTAACTCTGTC 507  
Db 424 TAACCTAATAGTGTAGTGTGTTGACGTTACCGAGATTAAGCAGTGAAGAGACACT 483  
QY 508 CAGCAGCGCGGTAAATACAGAGGTGCAAGCGTTAATCGGAATTAAGTTCGAGTGAAGAG 567  
Db 484 CAGCAGCGCGGTAAATACAGAGGTGCAAGCGTTAATCGGAATTAAGTTCGAGTGAAGAG 543  
QY 568 GCGT 627  
Db 544 GCGT 603  
QY 628 GAACCTGT 687  
Db 604 ARACTGT 663  
QY 688 CGT 747

Db	664	CGTAGATATAGGAAGGAAACCACTGCGGAAGCGACCACTGGACTGATCTGACACTG	723
QY	748	AGGCTCGAAAGCGTGGGTAGCAAAACAGATAGATACCCTGGTGTAGTCACGCGCTAAACG	807
Db	724	AGTGCGAAGCGTGGGAGCAACAGGATAGATACCTGGTAGTCCACGCGCTAAACG	783
QY	808	ATGCTACTAGTCGTGTGGTCCCTTGAGGACCTTAGTGACGAGCTAACGCAATAAGTAGA	867
Db	784	ATGTCAACTAGCCGTTGGAGCCCTTGAGCTCTTGTCGTCAGCTAACGCTTAGTGTGA	843
QY	868	CCGCTCGGGGATGACGGCCGCAAGGTTTAAATTCAAATGAATTGACGGGGGCCGCAAA	927
Db	844	CCGCTCGGGGATGACGGCCGCAAGGTTTAAATTCAAATGAATTGACGGGGGCCGCAAA	903
QY	928	CGGTGAGCAGTCGTTTAAATTCGATGCAAGCGCAAGCAACTTACCTGGTCTTGACATA	987
Db	904	CGGTGGAGCATGTGGTTTAAATTCGAAGCAAGCGCAAGCACTTACCAGGCTTGACATC	963
QY	988	CACAGATCTTGTAGAGATACGAGATGCTTCGGGAATTGTGATACAGTGTGTCATGG	1047
Db	964	CAATGACATTCACAGATGATGGTGTGCTTCGGGAACATTGACAGCTGCTGCATGG	1023
QY	1048	CTGTGCTGACGTCGTGCGTGAGATGTGGGTAAATCCGCAACGAGCGCAACCTTGT	1107
Db	1024	CTGTGCTGACGTCGTGCGTGAGATGTGGGTAAATCCGCAACGAGCGCAACCTTGT	1083
QY	1108	CCTTAGTACCAGCAC-TTCGGTGGGACTCTAGGATCTAGGATCTGCAAGCAACTGGAG	1166
Db	1084	CCTTAGTACCAGCACCTAATGTGGGCACTCTAAGAGACTGCGGTGCAAAACGGAG	1143
QY	1167	GAAGCGGGGACGACGTCACATCATGSCCCTTACGACGAGGCTACACAGCTGCTAC	1226
Db	1144	GAAGTGGGGATGACGTCAACTCAATGGCCCTTACGGCTTGGGCTTACACAGCTGCTAC	1203
QY	1227	AATGTAGGTACAGAGGCGACTACACGCGATGTGATCGGAATCTCAAAAAGCCTATCG	1286
Db	1204	AATGTGCGGTACAGAGGTTGCCAAGCGCGAGGTGGAGCTAATCCACAAAACCGATCG	1263
QY	1287	TAGTCACGATTTGGAGTCTGCAACTCGACTCCATGAAAGTAGGAAATCGTAGTAAATCGCGGA	1346
Db	1264	TAGTCGCGGATTCGCACTTGCACCTCGACTGCGTGAAGTCGGAATCGTAGTAAATCGCGGA	1323
QY	1347	TCAGATGCGCGGTGAATACGTTCCCGGGSCCTTGATACACACGCGCGTGCACACATGG	1406
Db	1324	TCAGATGTCGCGGTGAATACGTTCCCGGGSCCTTGATACACACGCGCGTGCACACATGG	1383
QY	1407	AGTTGATGCACCAAGATGGTTAGCCTAA-CTTAGTAGGGGCGATCACCAAGGTGTGGT	1465
Db	1384	AGTGGGTTGCACGAACCTAGCTAGTCTACCTTTCGGGAGGACGTTTACCAGGCTGTAT	1443
QY	1466	CGATGACTGGGTGAAGTCGTACACAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC	1523
Db	1444	TCATGACTGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC	1501

## RESULT 4

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US-09/745-476-1
; Sequence 1, Application US/09745476
; Patent No. 6521429
; GENERAL INFORMATION:
; APPLICANT: CANON INC.
; TITLE OF INVENTION: Preparation of Poly-hydroxyalkanoic Acid
; FILE REFERENCE: 4351008
; CURRENT APPLICATION NUMBER: US/09745,476
; CURRENT FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Microsoft word
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii p161 ; FERM P-17445
US-09-745-476-1

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QY      1407 AGTTGATTCACACAGAACTGGTTAGCCTTA--CTTAGTGAGGGCGCATCACACCGGTGTGGT 1465
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1384 AGTGGGTTCCACCAAGAAGTAGCTAGTCTAACCTTCGGGAGACGGGTACCACGGTGTGAT 1443
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      1466 CGATGACTGGGTGAAGTCGTACAAAGGTAGCCGTAGGGGAACCTGC GGCTGGATCAC 1523
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1444 TCATGACTGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACTCGGGCTGGATCAC 1501
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 6
US-08-114-695A-1
; Sequence 1, Application US/08114695A
; Patent No 5508193
; GENERAL INFORMATION:
; APPLICANT: Mandelbaum, Raphael T.
; APPLICANT: Wackett, Lawrence P.
; TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND
; TITLE OF INVENTION: WATER
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.
; STREET: 3500 IDS CENTER
; CITY: MINNEAPOLIS
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/114,695A
; FILING DATE: 31-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MUETING, ANN M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 600.268US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; US-08-114-695A-1

Query Match              70.5%; Score 1076; DB 1; Length 1542;
Best Local Similarity    67.2%; Pred. No. 0;
Matches 1008; Conservative 246; Mismatches 243; Indels 4; Gaps 3;

QY      30  GCCGCCAGGCTTACACATGCACAATCGACGGGAAACGATGA--TAGCTTGCTATTAGCGC 87
       ||||| |:| :||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      38  GCCGGCAGGCCUUAACAAGUCGAAACGCUAACACGGAAGAAAGAGUUGUUUUUUUUUU 97
       ||||| |:| :||::||::||::||::||::||::||::||::||::||::||::||:
QY      88  TCGAGCNCGCCGAGGGGTGAGTAATACTTAGGAATCTACTAGTAGTGGGGGATAGCTCG 147
       ||||| |:| :||::||::||::||::||::||::||::||::||::||::||:
Db      98  GACCAUGGCGGAGGGUGAGUAUUGUCUGGGAAACUUCGUUGAGGGGGGNARACUAC 157
       ||||| |:| :||::||::||::||::||::||::||::||::||::||::||:
QY     148  GGGAAATCSAATTAAATACCCCATACGCTTACGGGAGAAAGCAGGCGGNTCATTAGACCTT 207
       ||||| |:| :||::||::||::||::||::||::||::||::||::||::||:
Db     158  UGGAACGGVAGCURAUACCAGCAUCAAGUCGACAGACCAAGAGGGGGACCUCUGGGCCUC 217
       ||||| |:| :||::||::||::||::||::||::||::||::||::||::||:
QY     208  CCGCTATTAGATGACGCTTAAGCTCGATTAGCTAGTGTGGGGTAAAGAGCCATTACCATGCG 267
       ||||| |:| :||::||::||::||::||::||::||::||::||::||::||:
Db     218  UUGCCAUCGGAGUUGGCCAUGGAUGGAUUAGUAGUAGUGGGUUAACGCCUACCUAGGC 277
       ||||| |:| :||::||::||::||::||::||::||::||::||::||::||:

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1347 TCAGAAATCCGCGTGAATACGTTCCCGGGCTGTATACACACCGCCCTCACACCATGGG 1406  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1358 UCAGAAUGCCACGGGUAUAUCCUCCGGCCUUGUACACACCGCCGUCACCAUGGG 1417  
1407 AGTTGATGTCACAGAGAGTGGTATGACCTAA-CTTAGTGGAGGCGATCACACCGTGTGGT 1465  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1418 AGUGGUGUCAAAGAGAGUAGUAGCUAAUCCUCCGGAGGGCGCUUACCAUUGUAGU 1477  
1466 CGATGACTGGGTGAGTGGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1525  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1478 UCAAGACUGGGUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1537  
1526 C 1526  
1538 C 1538

## RESULT 7

US-08-757-653-158  
; Sequence 158, Application US/08757653  
; Patent No. 5843669  
; GENERAL INFORMATION:  
; APPLICANT: Kaiser, Michael W.  
; APPLICANT: Lyamichiev, Victor I.  
; APPLICANT: Lyamichiev, Natasha  
; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using  
; TITLE OF INVENTION: Thermostable FEN-1 Endonucleases  
; NUMBER OF SEQUENCES: 190  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Medlen & Carroll, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States Of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08757,653  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ingolia, Diane E.  
; REGISTRATION NUMBER: 40,027  
; REFERENCE/DOCKET NUMBER: FORS-02565  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 158:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1542 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-757-653-158

Query Match 70.1%; Score 1069.2; DB 2; Length 1542;  
Best Local Similarity 83.7%; Pred. No. 0;  
Matches 1256; Conservative 0; Mismatches 241; Indels 4; Gaps 4;  
QY 30 GCGCGAGGCTTAACATGCAAGTCGAGCGGAAC-GATGATAGCTTGTATAGGCGT 88  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 38 GCGCGAGGCTTAACATGCAAGTCGAGCGGAACGATGATAGCTTGTATAGGCGT 97  
QY 89 CGAGNCCGCGAGCGGTGAGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAGTAAT 148  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 98 ACAGTGGCGGCGGTGAGTAATAGTAATAGTAATAGTAATAGTAATAGTAATAGTAAT 157  
QY 149 GGAATCGAATTAATCCGCAT-ACGCTACGGGAGAAACCGGGGNTCAITTAGACCTT 207

158 GGAACGCTAGCTAATACCGCAFAACGTCGCAAGACCAAGAGGGGACCTTCGGGGCCTC 217  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 208 GGGCTATTAGATGAGCCCTAAGTCGGATTAGCTAGTAGTGGTGGGTAAGGCTTACCATGGC 267  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 218 TTGCCATCGGATGTGCCAGATGGATTAGCTAGTAGTGGGTAAGGCTTACCATGGC 277  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 268 GAGCATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGAGTGGAGACGACGCGCGG 327  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 278 GAGCATCCCTAGCTGGTCTGAGAGGATGACCGACCGACCTGGAATCTGAGACAGCTCCAG 337  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 328 ACT-CTACGGGAGGACGACGATGGGGAATATTGGACAATGNGNGGAACCTTGATCAGCA 386  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 338 ACTCTACGGGAGGACGACGATGGGGAATATTGCACATGGCGCAAGCCTGATGACGCA 397  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 387 TGGCGGTGTGTGAAGAAGGCTTTTGGTTGTAAGACACTTTAAGCAGTGAAGAAGACTC 446  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 398 TGCCCGTGTATGAAGAAGGCTTCGGGTTGTAAGTACTTTTCAGCGGGGAGGAAGGGAG 457  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 447 TTCGGTTAATACCGGGGACGATGACATTAAGTGCAGATAAGCACCGGCTACTCTGTG 506  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 458 TAAAGTTAATACCTTGTCTCATTGACGTTACCGCGAAGAGAACCGGCTACTCTCGTG 517  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 507 CCAGCAGCGCGGTAATACAGAGGTCGAAGCGTTAATCGGAATTACTGGGCGTAAAGCG 566  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 518 CCAGCAGCGCGGTAATACAGAGGTCGAAGCGTTAATCGGAATTACTGGGCGTAAAGCG 577  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 567 AGCTAGTGGCTTGATAGTCAAGTGTGAATCCCGGGCTTAACTGGGAATGTCATC 626  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 578 CAGCGACGCGGTTTGTAAAGTCAGATGTGAATCCCGGGCTCAACCTGGGAATGCTATC 637  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 627 TGAACCTCTAGGCTAGTAGTGGAGGAGTGAATTTTCAGGTGAGCGGTGAAT 686  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 638 TGATACTGGCAGCTGTAGTCTCGTAGAGGGGGGTAGAATTCAGGTGTAGCGGTGAAT 697  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 687 GCTAGAGATCTGAAGGAATACCGATGGCGAAGGAGCGCTTCTTGGCATCATCTACTGACAT 746  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 698 GCGTAGAGATCTGGAGGAATACCGGTGGCGAAGCGGCCCTTGACGAGACTGACGCT 757  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 747 GAGCTCGAAGCGTGGGTAGCAACAGATTAAGTATACCTTGGTAGTCACGCGGTAAC 806  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 758 CAGGTGCGAAGCGTGGGAGCAACAGGATTAGATACCTCTGGTAGTCCACGCGGTAAC 817  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 807 GATGCTACTAGCTGGTGGTCCCTTGAGGACTTAGTGACGACGCTAACCAATTAAGTAG 866  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 818 GATGCTAGCTTGGAGGTTGTGCCCTTGAGCGGTGGCTTCCGAGAGCTAACCGGTAAAGT 877  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 867 ACCGCTCGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATTACGCGGGGCCCGCA 926  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 878 ACCGCTCGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATTACGCGGGGCCCGCA 937  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 927 AGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACTGGTCTTGACAT 986  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 938 AGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACTGGTCTTGACAT 997  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 987 ACACGAATCTTGTAGAGATACGAGATGCTTCGCGGAATTGTGATACAGGTGCTCGATG 1046  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 998 CCACGGAAGTTTTCAGAGATGAGATGTGCTTCGCGAACCCTGAGACAGGTGCTCGATG 1057  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 1047 GCTGCTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTTGTG 1106  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1058 GCTGCTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTTGTG 1117  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 1107 TCCTTAGTTACGACATGTCGGGTGGGAATCTAGAGTACTGCCAGTGCACAACTGGAG 1166  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1118 TCCTTTGTCGCGGGTCCCGGGGAACTCAAAAGAGAGTGCAGTGTATAAATGAGAG 1177  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 1167 GAGGCGGGGAGCGAGCTCATCATGCGCTTACGCCAGGCTTACACAGCTGCTAC 1226  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1178 GAGGTGGGGATGAGCTCAAGTCAATGCGCTTACGACGAGGCTTACACAGCTGCTAC 1237  
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QY 1227 AATGGTAGTACAGAGGCGAGCTACACAGCATGTGATGCGAATCTCAAAAGCCTATCG 1286  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||





1347 TCAGAAATGCGCGGTGAATACGCTCCCGGCGCTTGTATACACACGCGCGCTFCACACCATGGG 1406  
1358 UCAGAAUGCCAGCGGUAUACUCCCGGCGUUGUACACACGCGCGUACACCAUUGG 1417  
1407 AGTTGATGACAGCAGAGTGGTTAGCTTAA-CTTAGTGGGCGGATFCACACGCGTGGT 1465  
1418 AGUGGUGUCAAAGAAGUAGUACUUAACUUCGCGGAGGCGCUUACCAUUGUAGU 1477  
1466 CGATGACTGGGCTGAGTCTGTAACAGATAGCCCTAGCGGAGACCTGCGGCTGGATFACCT 1525  
1478 UCAUGACUGGGUGAAGUCUACAAGGUAACCGUAGGGAACUUGGUGUUAUCCU 1537  
1526 C 1526  
1538 C 1538  
RESULT 9  
US-08-520-946-158  
; Sequence 158, Application US/08520946  
; Patent No. 6372424  
; GENERAL INFORMATION:  
; APPLICANT: BROW, MARY ANN D.  
; APPLICANT: LYAMICHEV, VICTOR I.  
; APPLICANT: OLIVE, DAVID M.  
; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
; TITLE OF INVENTION: PATHOGENS  
; NUMBER OF SEQUENCES: 160  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL  
; STREET: 220 MONTGOMERY STREET, SUITE 2200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,946  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: FORS-01756  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 158:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1542 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-520-946-158

Query Match 70.1%; Score 1069.2; DB 4; Length 1542;  
Best Local Similarity 83.7%; Pred. No. 0;  
Matches 1256; Conservative 0; Mismatches 241; Indels 4; Gaps 4;  
QY 30 GCGCGCAGGCTTACACATGCAAGTCAGCGGGAAC-GATGATAGTTCTCTATTAGGGGT 88  
DB 38 GCGCGCAGGCTTACACATGCAAGTCGAAAGCTACAGAGAAAGCTTCTCTTTTGGTG 97  
QY 89 CGAGCNGCCGAGCGGTGAGTATACCTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGG 148  
DB 98 AGGAGTGGCGGAGCGGTGAGTATGCTGGGAAACTGCTGATGGAGGGGATAGTACT 157  
QY 149 GGAAGTGAATTAACCGCAT-ACGCTACGGGAGAAAGCAGGGGNTATTAGACCTT 207

DB 158 GGAACGGTAGCTAATACCATACGCTCGCAAGACCAAGAGGGGAGCTTCGGGCGCTC 217  
QY 208 GCGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGCTGGGTGAAGGCTTACCATGGC 267  
DB 218 TTGCCATCGGATGTGCCAGATGGGATTAGCTAGTGGGTGAGGCTCACCTAGGC 277  
QY 268 GACGATCTGTAGTGTCTGTAGAGGATGATCAGCCACACCGGAGCTGAGACGCGCCGG 327  
DB 278 GACGATCCTAGCTGTCTGTAGAGGATGACAGCCACACTGGAACCTGAGACACGGTCCAG 337  
QY 328 ACT-CTACGGGAGGACGACGCTGGGAATATTGGCAATGNGGGAACCTGATCCAGCA 386  
DB 338 ACTCTACGGGAGGACGCTGGGAATATTGGCAATGNGGGAACCTGATCCAGCA 397  
QY 387 TCCGCGCTGTGTGAAGAAGGCTTTTGGTTGTAAAGCACTTAAAGCAGTGAAGAAGACT 446  
DB 398 TCCGCGCTGTATGAAGAAGGCTTTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAGGAG 457  
QY 447 TTCGGTTAATACCGGGGAGGATGACATTAGCTGCAGAAATAAGCACCAGGCTACTCTGTG 506  
DB 458 TAAAGTTAATACCTTGTCTCATTTGACGTTACCCCGCAAGAAGACCGGCTACTCCGTG 517  
QY 507 CCAGCAGCGCGGTAAATACAGAGGCTGCAAGCGTTAAATCGGAATTACTGGGCTTAAAGCG 566  
DB 518 CCAGCAGCGCGGTAAATACAGAGGCTGCAAGCGTTAAATCGGAATTACTGGGCTTAAAGCG 577  
QY 567 AGCGTAGGTGGCTTGTAAAGTACAGATGTGAATCCCGGGCTTAACTGGGAACTGCATC 626  
DB 578 CACGACGCGGTTTGTAAAGTACAGATGTGAATCCCGGGCTCAACTGGGAACTGCATC 637  
QY 627 TGAAGTCTTAGCTAGCTAGTGTGAGAGGGAAGTAGAATTCAGGTGTAGCGGTGAAT 686  
DB 638 TGATACTGGCAAGCTTGTAGTCTGTAGAGGGGGGTAGAAATTCAGGTGTAGCGGTGAAT 697  
QY 687 GGTAGAGATCTGAAGGAATACGATGCGAAGGAGCTTCTTGGCATCAATACTGACACT 746  
DB 698 GGTAGAGATCTGGAGGAATACGCTGGGAGGCGGCCCTTGGAGAGAACTGACGCT 757  
QY 747 GAGGCTGAAAGCGTGGGTAGCAACAGATAGATACCTGTGTAGTCCACCGCTAAAC 806  
DB 758 CAGGTGCGAAAGCGTGGGAGCAACAGGANTAGATACCTTGTAGTCCACCGCTAAAC 817  
QY 807 GATGTCTACTAGTGTGGTCCCTGTAGGACTTAGTACGACGCTAAGCAATAGTAG 866  
DB 818 GATGTGACTTGGAGGTTTGCCCTTGTAGCGGTGGCTTCCGAGCTACGCGTTAGTCG 877  
QY 867 ACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAATGAATGACGGGCGCGGCA 926  
DB 878 ACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAATGAATGACGGGCGCGGCA 937  
QY 927 ACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAATGAATGACGGGCGCGGCA 986  
DB 938 ACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAATGAATGACGGGCGCGGCA 997  
QY 987 ACACAGAACTCTGTAGAGATACGAGATGCTTGGGGAATTTGTATACAGGTGCTGCATG 1046  
DB 998 CCACGGAAGTTTTCAGAGATGAGATGTCCTTGGGACCGGTGAGACAGGTGCTGCGATG 1057  
QY 1047 GCTGTGCTAGCTGCTGTGAGATGTTGGGTTAAGTCCCGCAAGCAGCGCAACCCCTTG 1106  
DB 1058 GCTGTGCTAGCTGCTGTGAGATGTTGGGTTAAGTCCCGCAAGCAGCGCAACCCCTTA 1117  
QY 1107 TCTTAGTTACCACTCGGCTGGGTAATCTTAGGATGATGCTGCAAGTGAACCTGAG 1166  
DB 1118 TCTTTTGTTCAGCGGTCGCGCGGAACTCAAGGAGACTGCCAGTGAATTAAGTGGAG 1177  
QY 1167 GAAGCGGGGAGGACGCTAAGTCAATCCTTACGACCGGCTACACAGCTGCTAC 1226  
DB 1178 GAAGTGGGATGACGCTAAGTCAATCCTTACGACCGGCTACACAGCTGCTAC 1237  
QY 1227 AATGTAGTACAGGCGGAGCTACAGCGATGTGATGGAATCTCAAAAAGCCTATCG 1286







QY	1345	GATCAG-AATGCCGGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCAACCAAT	1403
Db	1354	GATCAGCATTTGTGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCAACCAAT	1413
QY	1404	GGAGTGTATTGCACAGAACTGTTAGCTAA-CTTAGTCAGGGCGGATCACCACGGGTGT	1462
Db	1414	GGAGTTTGTTCACACAGACAGGTAAGCTTACGCCAAGGGGGCGCTTGCCACGGGTGT	1473
QY	1463	GGTCGATGACTGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGTGGATCA	1522
Db	1474	GGCCGATGACTGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGTGGGTGGATCA	1533
QY	1523	CCCTC	1526
Db	1534	CCCTC	1537

RESULT 12  
 US-09-967-376-1  
 ; Sequence 1, Application US/09967376  
 ; Patent NO. 6482635  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WALKER, Harrell L.  
 ; APPLICANT: HIGGINBOTHAM, Lawrence R.  
 ; TITLE OF INVENTION: CONTROL OF CYANOBACTERIA WITH A BACTERIUM  
 ; FILE REFERENCE: 013243-0007  
 ; CURRENT APPLICATION NUMBER: US/09/967,376  
 ; CURRENT FILING DATE: 2001-09-28  
 ; NUMBER OF SEQ ID NOS: 1  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 1540  
 ; TYPE: DNA  
 ; ORGANISM: Unknown Organism  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Unknown Organism: Bacterium SG-3; gram negative;  
 ; OTHER INFORMATION: rod-shaped; exhibits flagellate motility; pathogenic to  
 ; OTHER INFORMATION: cyanobacteria and algae; yellow colonies on BG-11 medium suppl.  
 ; OTHER INFORMATION: with tryptic soy  
 US-09-967-376-1

QY	447	TTCGGTTAATACCCCGGAGCATGACATTAAGTCTGCAGAAATAAGCACCGGTACTCTCTGTG	506
Db	454	CTGGATTAAATCTTCGGTGTTCTCAGCGGTACCGGAAGAATAAGCACCGGTACTCTCTGTG	513
QY	507	CCAGCAGCCGGSTAAATACAGAGGGTGCAGGTTAAATCGGAATTAATCTGGCGGTAAACGG	566
Db	514	CCAGCAGCCGGGTAAATACAGAGGGTGCAGGTTAAATCGGAATTAATCTGGCGGTAAACGG	573
QY	567	AGCGTAGGTGGCTTGATAAGTCAAGATGTGAAATCCCCGGGCTTAACCTGGGAACATGCAATC	626
Db	574	TGCGTAGGTGGTTCGTTAAGTCTGATGTGAAAAGCCCTGGGCTCAACCTGGGAATTCGCAAT	633
QY	627	TGAACCTGTTAGGCTAGTAGTAGTAGAGAGGAACTAGAAATTTAGGTAGTAGCGGTGAAT	686
Db	634	GGAATATGGCGGGCTAGAGTCGGTAGAGATGGCGGAATTCOCGGTGTAGCAGGTGAAT	693
QY	687	CGGTAGAGATCGAAGGAATAACCGATGGCGAAGGAGAGCTTCCTGGCATCATACTGACACT	746
Db	694	CGGTAGAGATCGGAGGAGAACATCTGTGGCGAAGGCGCCATCTGACCAGCAGCTGACACT	753
QY	747	GAGGCTCGAAAGCTGGGTAGACAACAAGATTAGATACCCCTGGTAGTGTGCCAGCGCTAAAC	806
Db	754	GAGGACGAAAGCGTGGGGGCAACAAGATTAGATACCCCTGGTAGTGTGCCAGCGCTAAAC	813
QY	807	GATGTCCTACTGCTGTGGGTCCCCTTGAGG - ACTTAGTGAAGCAGAGCTTAAGCGAAATAAGTA	865
Db	814	GATCGNACTGGATGTTGGGTGCAACTAGGCACCTCAGTATCGRAGCTTAGCGGTTAAGTT	873
QY	866	GACCGCTGGGAGTAGCGCGCGCAAGGTTTAAACTCAAATGAATTAAGTGAAGCGGCGCGCAC	925
Db	874	CGCCGCTGGGAGTAGCGTGCAGAACTGAAACTCAAAGGAATTAAGCAGGCGGCGCGCAC	933
QY	926	AAGCGGTGAGGACTGTGTTTTAATTCGATGCAACGCGAAGAACCTTACCTTGCTTGTGACA	985
Db	934	AAGCGGTGAGGATTGTGTTTTAATTCGATGCAACGCGAAGAACCTTACCTTGCTTGTGACA	993
QY	986	TACACAGAATCTTTAGAGATACAGAGAGTGCCTTCGCGAATTTGTGATPACAGGTGCTGCAT	1045
Db	994	TGCACAGGAATCTTCAGAGATAGGATTCGTCGCTTCGCGAACCCTGACACAGTGTGCTGCT	1053
QY	1046	GGCTGTGCTCACTGCTCTGCTGAGATGTGGTAACTCCCGCAAGCAGCGCAACCCCTT	1105
Db	1054	GGCTGTGCTCAGCTCGTGTGCTGAGATTTGGTTAAGTCCCGCAAGCAGCGCAACCCCTT	1113
QY	1106	GTCCTTAGTTTACCAGCAC - TTCGGGTGGGAAGTCTAAGGATAGTGCACAGTGCACAACATGG	1164
Db	1114	GTCCTTAGTTTACCAGCACATATGGTGGGAAGTCTAGGAGACCGCGCGGACAAAGCCGG	1173
QY	1165	AGGAGCGCGGAGACGCTCAAGATCATATGGCCCTTAGCBACAGGCTTACACAGTGTCT	1224
Db	1174	AGGAGGTGGGGATGACGTCAAGTCAATGTCATGTCGCGCCCTTAGCGCCAGGCTTACACAGT	1233
QY	1225	ACAATGTAGTGTACAGAGGCGACGTACACAGGAGTGTGATCGAATCTCAAAAAGCCTAT	1284
Db	1234	ACAATGTGGGACAGAGGGCTGCAAACTCGCGAGAGTGAAGCAATCCCAAGAAACCCAT	1293
QY	1285	CGTAGTCCAGATTGAGTCTCCACTCGACTCCATGAAGTAGGAATCGCTAGTAAATCCGG	1344
Db	1294	CTCAGTCCGGATTGAGTCTCCACTCGACTCGACTCGATCGATGAAGTGGGAATCGCTAGTAAAT	1353
QY	1345	GATCAG - AATGCGCGGGTGAATAGTTCGCGGGCCCTTGTACACACCGCCGTCACACCAT	1403
Db	1354	GATCAGCATTTGCTCGGGTGAATAGTTCCCGGGCCCTTGTACACACCGCCGTCACACCAT	1413
QY	1404	GGGATTTGATTCACAGAGTGGTTAGCCCTAA - CTTTAGTAGGGGCGGATCAACACGGTGT	1462
Db	1414	GGGATTTGTTGCACCAAGCAGGTAGCTTAACCGCAAGGGGGGGCGCTTGGCCAGGGTGT	1473
QY	1463	GGTCGATGACTGGGTGAAGTCGTAACAGAGTAGCCGTAGGGAACCTCGCGGCTGGATCA	1522
Db	1474	GGCCGATGACTGGGGTGAAGTCGTAACAGAGTAGCCGTATCGGRAGGTGCGGTTGGATCA	1533
QY	1523	CCTC 1526	

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Db      1534 CCTC 1537
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RESULT 13
US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1
Query Match      66.18; Score 1008.8; DB 4; Length 1830121;
Best Local Similarity 81.68; Pred. No. 0;
Matches 1225; Conservative 0; Mismatches 270; Indels 6; Gaps 5;
QY      30  GCGGCGAGCTTAACACATCAAGTCCGAGCGAAAC-GATGATAGCTTGTCTATTAGGCGT 88
Db      770649  GCGGCGAGCTTAACATCAAGTCCGAGCGTACGAGGAAGTCTGCTTCTGCTG 770708
QY      89  CGAGNCGCGGAGCGGTGAGTAATCTAGGAATCTACTAGTAGTGGGGGATAGCTCGG 148
Db      770709  ACGAGTGGCGGACGGGTGAGTAATGCTTGGGAATCTGCTTATGAGGGGGATACGAGC 770768
QY      149  GGAACACTGAATTAATACCCGATA-CGTCTACGGGAGAAACGAGGGGNTCATAGACCTT 207
Db      770769  GGAACACTGCTCAATACCCGCTATTATCGGAAGATGAAGTTCGGGACTGAGAGGCGC 770828
QY      208  GCGCTATTAGATGAGCCCTAAGTCGATAGCTAGTGTGGGTAAAGGCTACCATGSC 267
Db      770829  ATGCCATAGATGAGCCCAAGTGGGATAGTAGTGTGGGGTAAATGCTTACCAAGCC 770888
QY      268  GACGATCTCTAGCTGGTCTGAGAGGATGATCAGCCACACCGGACTGAGACACGGCCGG 327
Db      770889  TGGGATCTCTAGCTGGTCTGAGAGGATGATCAGCCACACCGGACTGGAACACTGAGACACGGTCCAG 770948
328  ACT-CTACGGGAGGACGACGTGGGGAATATTGACCAATGNGGGAACCCCTGATCCAGCA 386
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
770949  ACTCTACGGGAGGACGACGTGGGGAATATTGCGCAATGNGGGAACCCCTGACGACCA 771008
QY      387  TCCCGCGTGTGTGAAGAAGCCCTTTTGGTTGTAAAGCACCTTTAAGCAGTGAAGAAGACTC 446
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
771009  TCCCGCGTGAATGAAGAAGCCCTTCCGGTGTGTAAAGTTCCTTCGGTATTGAGGAAGTTG 771068
QY      447  TTCGGTTAATACCCCGGAGCGATGACATTAGCTGCAGANAATAGCAGCGCTAATCTCTG 506
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
771069  ATGTCTTAATAGTACATAAAATTGACGTTAAATACAGAGAAGACCGGCTAACCTCCG 771128
QY      507  CCAGCAGCGCGGCTAATACAGAGGCTCAAGCGTTAATCGGAATTAATCGGCTAAAGCG 566
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
771129  CCAGCAGCGCGGTAATACCGAGGCTGCGAGGCTTAATCGGAATTAATCGGCTAAAGCG 771188
QY      567  ACGTAGTGGCTTGATAGTACATGTAATCCCGGGCTTAACCTCGGAACTGCAATC 626
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
771189  CACGCGGCGGTATTATTAAGTGAGGTGTAAAGCCCTGGGCTTAACCTAGGAATTCATT 771248
QY      627  TGAACCTGTAGGCTAGATAGTGTGAGAGGAGTAGAATTTAGTGTAGCGGTGAAT 686
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
771249  TCAGACTGGTAATAGGACTTATTAGGAGGGGTAGAAATTCACGCTGAGCGGTGAAT 771308
QY      687  GCGTAGATCTGAAGGAATACCGATGCGAAGCGAGCTTCCTGGCATCATACTGACACT 746
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
771309  GCGTAGATCTGAGGAATACCGAAGCGAGGAGCGCCCTTGGGAATCTACTGACGCT 771368
QY      747  GAGGCTCGAAGCGTGGGTAGCAACAGGATTAGTACCTTGTGTAGTCCACGCGGTAAAC 806
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
771369  CATGTGCGAAGCGTGGGAGCAACAGGATTAGTACCTTGTGTAGTCCACGCTGTAAAC 771428
QY      807  GATGCTACTAGTGTGGTCCCTTGAGAGCTTGTAGCGAGCTAAGCCATACATAGTAG 866
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
771429  GCTGTCGATTTGGGATTTGGG--CTTAGAGCTTGTGCCCCCTAGCTAACGTGTAATCT 771486
QY      867  ACCGCTGGGAGTACGCGCGCAAGGTAAAACTCAATGAATTTAGCGGGGGCCGACACA 926
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
771487  ACCGCTGGGAGTACGCGCGCAAGGTAAAACTCAATGAATTTAGCGGGGGCCGACACA 771546
QY      927  ACGGCTGGAGCATGTGTTTAATTCGATCAACGGGAAGAACCTTACTCGTCTTGACAT 986
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
771547  ACGGCTGGAGCATGTGTTTAATTCGATCAACGGGAAGAACCTTACTCGTCTTGACAT 771606
QY      987  ACACAGATCTTTAGAGATACGAGAGTGCCTTCGGGAATTTGTATACAGTGTCTCATG 1046
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
771607  CCTAAGAAGACTCAGAGATGAGCTTGTGCTTCGGGAATTTAGAGAGAGTGTCTCATG 771666
QY      1047  GCTGTCGTCAGCTGCTGTCGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTG 1106
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
771667  GCTGTCGTCAGCTGCTGTCGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTA 771726
QY      1107  TCTTAGTTTACCAGCACTTCGGTGGGAACTCTAAGGATATCTGCCAGTGAACAACTGG 1166
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
771727  TCTTTTGTTCAGCAGCTTGGTGGGAACTCAAAGGAGACTGCCAGTGAATAAAGTGGAG 771786
QY      1167  GAGGCGGGGAGCGCTCAAGTCAATCATGGCCCTTACGACCGAGGCTTACACAGTGTCT 1226
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
771787  GAGGCTGGGAGTACGCTCAAGTCAATCATGGCCCTTACGAGTAGGGCTTACACAGTGT 771846
QY      1227  AATGCTAGTACAGAGGAGCTACACAGCATGTGATGCGGAATCTCAAAAGACCTTATCG 1286
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QY      1287  TAGTCAGATTTGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAAATCGCG 1346
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QY      1347  TCAGAAATCGCGGTTGAATAGTTCCTCGGCGCTTTGTACACACCGCGCTCACACCAAT 1406
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771967  TCAGAAATCGCGGTTGAATAGTTCCTCGGCGCTTTGTACACACCGCGCTCACACCAAT 772026
QY      1407  AGTTGATTCCACCAGAGTAGTGGTTAGCTTA--CTTAGTAGGGGCGATCACCCACGGTGT 1465
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Db 126827 AAGTCGGGATGAGTCTCAACTCGACTCCATGACTCGAATCCCTAGTAATCGCAA 126768  
QY 1347 TCAGAAATCCCGGTGAATAGTTCOCGGGCTTGTACACACCGCCGTCACACATGGG 1406  
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QY 1466 CGATGACTGGGTTGAAGTCTGAACAGGTAGCCGTAGGGGAACCTTCGGCTGGATCACT 1525  
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QY 1526 C 1526  
Db 126587 C 126587

RESULT 15

US-09-643-990A-1

Sequence 1, Application US/09643990A

Patent No. 6528289

GENERAL INFORMATION:

APPLICANT: Robert D. Fleischmann

Mark D. Adams

Owen White

Hamilton O. Smith

J. Craig Venter

Matches 1225; Conservative 0; Mismatches 270; Indels 6; Gaps 5;  
QY 30 GCGCGCAGCTTAACACATCAAGTCGAGCGGAAC-GATGATAGCTTCTATTAGCGT 88  
Db 770649 GCGCGCAGCTTAACACATCAAGTCGAGCGGAAC-GATGATAGCTTCTATTAGCGT 770708  
QY 89 CGAGCNGCCGACGGGTGAGTAATCTAGTAAGTAATCTAGTAAGTGGGGGATAGCTCGG 148  
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QY 208 GCGCTATTAGATGAGCCCTAAGTCGATTAGTGTGGTAAAGCCCTACCATGGC 267  
Db 770829 ATGCCATAGGATGAGCCCTAAGTCGATTAGTGTGGTAAAGCCCTACCATGGC 770888  
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QY 328 ACT-CTACGGGAGGACGAGTGGGGAATATTGGACAATGNGGGGAACCCCTGATCAGCA 386  
Db 770949 ACTCTACGGGAGGACGAGTGGGGAATATTGGACAATGNGGGGAACCCCTGATCAGCA 771008  
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QY 927 ACGGTGAGCATGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 986  
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Query Match 56.1%; Score 1008.8; DB 4; Length 1830121;  
Best Local Similarity 81.6%; Pred. No. 0;





GenCore version 5.1.6  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1098.6	72.0	1501	9 US-09-791-592-1	Sequence 1, Appli
2	1098.6	72.0	1501	9 US-09-745-476-1	Sequence 1, Appli
3	1098.6	72.0	1501	9 US-09-821-016-5	Sequence 5, Appli
4	1098.6	72.0	1501	9 US-09-748-205-1	Sequence 1, Appli
5	1098.6	72.0	1501	9 US-09-793-920A-1	Sequence 1, Appli
6	1098.6	72.0	1501	10 US-09-951-720-1	Sequence 1, Appli
7	1098.6	72.0	1501	11 US-09-791-610-1	Sequence 1, Appli
8	1098.6	72.0	1501	14 US-10-218-519-5	Sequence 5, Appli
9	1098.6	72.0	1501	14 US-10-266-787-5	Sequence 5, Appli
10	1098.6	72.0	1501	14 US-10-252-518-5	Sequence 5, Appli
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13	1090.4	71.5	1494	13 US-10-007-725-5	Sequence 5, Appli
14	1073.8	70.2	1481	9 US-09-737-297-4	Sequence 4, Appli
15	1070.8	70.2	1467	9 US-09-726-774-3	Sequence 3, Appli
16	1070.6	70.2	1541	9 US-09-027-439-7	Sequence 7, Appli

17 1069.2 70.1 1542 11 US-09-940-925A-158 Sequence 158, App

18 1069.2 70.1 1542 11 US-09-941-193A-158 Sequence 158, App

19 1069.2 70.1 1542 14 US-10-061-071-33 Sequence 33, Appli

20 1062.6 69.6 1541 9 US-09-726-774-2 Sequence 2, Appli

21 1058.2 69.3 1549 9 US-09-912-020-89 Sequence 89, Appli

22 1058.2 69.3 1549 9 US-09-913-020-242 Sequence 242, App

23 1058.2 69.3 1549 9 US-09-912-020-402 Sequence 402, App

24 1052.4 69.0 1487 9 US-09-726-774-14 Sequence 14, Appli

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26 1046.8 68.6 1424 14 US-10-007-527A-12 Sequence 12, Appli

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28 1044.2 68.4 1506 9 US-09-027-439-3 Sequence 6, Appli

29 1037.8 68.0 1532 13 US-10-007-725-6 Sequence 4, Appli

30 1032.2 67.6 1505 9 US-09-027-439-4 Sequence 4, Appli

31 1031.2 67.6 1500 9 US-09-726-774-4 Sequence 1, Appli

32 1027.8 67.4 1486 9 US-09-737-297-1 Sequence 1, Appli

33 1025.2 67.2 1544 9 US-09-726-774-5 Sequence 5, Appli

34 1021 66.9 1505 9 US-09-027-439-6 Sequence 6, Appli

35 1019.8 66.8 1540 10 US-09-967-376-1 Sequence 1, Appli

36 1019.8 66.8 1540 14 US-10-260-847-1 Sequence 1, Appli

37 1016.4 66.6 1429 10 US-09-934-868-81 Sequence 81, Appli

38 1014.8 66.5 640681 10 US-09-790-988-1 Sequence 1, Appli

39 1008.8 66.1 1830121 14 US-10-329-960-1 Sequence 1, Appli

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43 979.8 64.2 1447 10 US-09-848-727-1 Sequence 1, Appli

44 961.8 63.0 1487 9 US-09-726-774-13 Sequence 13, Appli

45 854.6 56.0 1552 10 US-09-974-300-8479 Sequence 8479, Ap

## ALIGNMENTS

## RESULT 1

US-09-791-592-1  
; Sequence 1, Application US/09791592  
; Patent No. US20010021223A1  
; GENERAL INFORMATION:  
; APPLICANT: Canon Inc.  
; TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxybenzoylalkanoic acid  
; FILE REFERENCE: 4396021  
; CURRENT APPLICATION NUMBER: US/09/791,592  
; CURRENT FILING DATE: 2001-02-26  
; NUMBER OF SEQ ID NOS: 1  
; SEQ ID NO 1  
; LENGTH: 1501  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii 161 strain.  
US-09-791-592-1

Query Match 72.0%; Score 1098.6; DB 9; Length 1501;  
Best Local Similarity 85.9%; Pred. No. 2.3e-289;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

QY 30 GCGCGAGCTTACACATGTCGAGCGGAAACGATGATAGCTGCTATAGGCGTC 89  
Db 9 GCGCGAGCTTACACATGTCGAGCGGAAACGATGATAGCTGCTATAGGCGTC 66  
QY 90 GAGNCGCGGAGCGGTGAGTAACTACTAGGAATCTACTAGTGGGGATAGCTCGG 149  
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QY 150 GAACTCGAATTAATACCGCATACGT-CTACGGGAGAAACAGCGGNNWCATTAGACCTTG 208  
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Db 184 CGCTATCATAGTACGCTTACCTAGTGGATAGCTAGTATGGTGGGTAAAGGCTTACCATGCGC 243  
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RESULT 2  
US-09-745-476-1  
; Sequence 1, Application US/09745476  
; Patent No. US20010029039A1  
; GENERAL INFORMATION:  
; APPLICANT: CANON INC.  
; TITLE OF INVENTION: Preparation of Poly-hydroxyalkanoic Acid  
; FILE REFERENCE: 4351008  
; CURRENT APPLICATION NUMBER: US/09/745,476  
; CURRENT FILING DATE: 2000-12-26  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 1  
; TYPE: DNA  
; LENGTH: 1501  
; ORGANISM: Pseudomonas jessenii P161 ; FERM P-17445  
US-09-745-476-1

Query Match 72.0%; Score 1098.6; DB 9; Length 1501;  
Best Local Similarity 85.9%; Pred. No. 2.3e-289;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

QY 30 GCGCGGACGCTTAACACATGCAAGTCGAGCGGAAACGATGATGCTTATTAGGCGTC 89  
Db 9 GCGCGGACGCTTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTCTCTGAATCA 66  
QY 90 GAGGCGCGGAGCGGTGAGTAACTTATGGAATCTACCTAGTGTAGTGGGATAGTCTCGG 149  
Db 67 G---CGGCGGACGCGGTGAGTAACTGCTTAGGAATCTGCTTAGGAATCTGCTTAGG 123  
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Db 124 GAAAGGACGCTAATACCGCATACGTCTACGGGAGAAAGACAGGGGACCTTCGGGCGTTG 183  
QY 209 CGCTATTAGATGAGCTTAAGTTCGATTAAGTATGATGCTGCTTAAAGCTTACCATGGCG 268  
Db 184 CGCTATCAGATGAGCTTAAAGTTCGATTAAGTATGATGCTTAAAGCTTACCATGGCG 243  
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QY 329 CT-CTACGGGAGCAGTGGGGAATATTGGAATATTGGAATATTGGAATATTGGAATATTG 387  
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RESULT 5  
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; Sequence 1, Application US/09793920A  
; Patent No. US20020065389A1  
; GENERAL INFORMATION:  
; APPLICANT: Canon Inc.  
; TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxythienylalkanoic acid as  
; FILE OF INVENTION: monomer unit, and method for producing the same.  
; FILE REFERENCE: 4396021  
; CURRENT APPLICATION NUMBER: US/09/793,920A  
; CURRENT FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 1  
; SEQ ID NO 1  
; LENGTH: 1501  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii 161 strain.  
US-09-793-920A-1

Query Match 72.0%; Score 1098.6; DB 9; Length 1501;  
Best local similarity 85.9%; Pred. No. 2.3e-289;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

QY 30 GCGCGACGCTTAACATGCAAGTCGAGCGGAGAACGATAGTCTATTAAGGCTC 89  
DB 9 GCGCGACGCTTAACATGCAAGTCGAGCGGAGAACGATAGTCTATTAAGGCTC 66  
QY 90 GAGCNGCCGACGCGGTGAGTAACTTAGGAATCTACTAGTGTGGGATAGTCTGG 149  
DB 67 G---CGGCGACGCGGTGAGTAACTTAGGAATCTACTAGTGTGGGATAGTCTGG 123  
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DB 184 CGCTATTAGATGACCTTAAGTCGATAGTGTGGGATAGTGTGGGATAGTGTGGG 243  
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DB 244 AGATCTAGTCTAGTCTGAGAGGATGATCAGCACACCGGACTGAGACACGCGCCGGA 303  
QY 329 CT-CTACGGGAGGACGAGTGGGAAATATGGAATATGGAATATGGAATATGGAAT 387  
DB 304 CTCTCTACGGGAGGACGAGTGGGAAATATGGAATATGGAATATGGAATATGGAAT 363  
QY 388 GCGCGCTGTGTAAGAGGCTTTGGTGTAAAGCACTTTAGCAGTGAAGAAACACTCT 447  
DB 364 GCGCGCTGTGTAAGAGGCTTTGGTGTAAAGCACTTTAGCAGTGAAGAAACACTCT 423  
QY 448 TCGGTAAATCCCGGACGATGACATAGTCTGAGAAATAGCACCGGCTACTCTGTC 507  
DB 424 TACCTATAGTGTAGTGTGACCTTACCGACAGATAGCACCGGCTACTCTGTC 483  
QY 508 CAGCAGCGCGGTAAATACAGAGGTGCAAGCGTAAATCGGAATTAATCGGCTTAAGCGA 567  
DB 484 CAGCAGCGCGGTAAATACAGAGGTGCAAGCGTAAATCGGAAATTAATCGGCTTAAGCGC 543

QY 568 GGTAGTGGCTTGTATAGTCAATCTGAATCCCGGCTTACCTGGGAATCGATCT 627  
DB 544 GGTAGTGGCTTGTATAGTCAATCTGAATCCCGGCTTACCTGGGAATCGATCT 603  
QY 628 GAAATCTGTAGCTAGTGTAGAGGAGTGAATTTACGTTGTAGCGTGAATG 687  
DB 604 AATCTGTACAGCTAGTGTAGAGGAGTGAATTTACGTTGTAGCGTGAATG 663  
QY 688 CTTAGAGATCTGAAGGATACCGATCGGAGGAGTCTTCTGGCATCATCTAC 747  
DB 664 CTTAGATATAGAGGAGTACAGTGTGGAGGAGTCTTCTGGCATCATCTAC 723  
QY 748 AGCTCGAAGGCTGGGTAGCAACAGGATTAATACCTGCTGTAGTCCAGCGTAAAG 807  
DB 724 AGTGGGAGGCTGGGAGTGAATTAATTCGATGATGATGATGATGATGATG 783  
QY 808 ATGTCTACTAGTCTGGGCTCCCTTGGAGCTTGTAGCAGCTACGCAATTAAGT 867  
DB 784 ATGTCAACTAGCTGTGGAGCTTGTAGCTTGTAGTGGCAGCTAACGATTAAGT 843  
QY 868 CGCTGTGGGAGTACGCGCCGAAAGGTTAACTCAATGAATTCAGCGGCGCCGCA 927  
DB 844 CGCTGTGGGAGTACGCGCCGAAAGGTTAACTCAATGAATTCAGCGGCGCCGCA 903  
QY 928 GCGGTGGAGCATGTGGTTTAACTTCGATGCAACGCGAGAACCTTACCTGTGTG 987  
DB 904 GCGGTGGAGCATGTGGTTTAACTTCGAGCAACGCGAGAACCTTACCTGTGTG 963  
QY 988 CACAGAACTTTGTAGATACGAGTGTCTTTCGGGAATTTGTATACAGTGTGTG 1047  
DB 964 CAATGAACCTTTCCAGAGATGATGGTGTCTTTCGGGACATTTGAGACAGTGTG 1023  
QY 1048 CTGTCTGAGTCTGTGTGATGATTTGGTTAAGTCCCGCAACGAGCGCAACCTGT 1107  
DB 1024 CTGTCTGAGTCTGTGTGATGATTTGGTTAAGTCCCGCAACGAGCGCAACCTGT 1083  
QY 1108 CTTAGTTACCGACAC-CTTCGCTGGGAACTCTAAGGAGTCTTACCGAGCTTAC 1166  
DB 1084 CTTAGTTACCGACACCAATTTGGTGGGACTCTAAGGAGTCTTACCGAGCTTAC 1143  
QY 1167 GAAGCGGCGACGCTCAAGTCTATCGGCTTTCAGCAGCGGCTTACACAGTGTCT 1226  
DB 1144 GAAGTGGGAGTCAAGTCTATCATGCTTTCAGGCTTTCAGGCTTACACAGTGTCT 1203  
QY 1227 AATGTGTAGTACAGAGGCTTCCCAAGCGGAGTGGAGCTTAATCCCAAAAACG 1286  
DB 1204 AATGTGTAGTACAGAGGCTTCCCAAGCGGAGTGGAGCTTAATCCCAAAAACG 1263  
QY 1287 TAGTCCAGATTTGGATCTGCAACTCGACTTCCATGAAGTAGGAATCGCTAGT 1346  
DB 1264 TAGTCCAGATTTGGATCTGCAACTCGACTTCCATGAAGTAGGAATCGCTAGT 1323  
QY 1347 TCAGAAATCCCGGTGAATACGTTCCCGGCTTGTATACACACCGGCTTACACCAT 1406  
DB 1324 TCAGAAATCCCGGTGAATACGTTCCCGGCTTGTATACACACCGGCTTACACCAT 1383  
QY 1407 AGTGTGATTCGACCAAGATGTTAGCTTAA-CTTGTAGTGGGCGGATCACCGGTGT 1465  
DB 1384 AGTGTGATTCGACCAAGATGTTAGCTTAA-CTTGTAGTGGGCGGATCACCGGTGT 1443  
QY 1466 CGATGACGCTGGTGAAGTCTGTCAGTGTAGCGTGTAGGAGAACCTCGGCTGAT 1523  
DB 1444 TCATGACTGGGTGAATCTGATCAAGGTAGCCGTAGGGGAACTCGCGCTGGATC 1501

RESULT 6  
US-09-951-720-1  
; Sequence 1, Application US/09951720  
; Patent No. US20020160467A1  
; GENERAL INFORMATION:  
; APPLICANT: Canon Kabushiki Kaisha  
; TITLE OF INVENTION: Polyhydroxyalkanoate and Manufacturing Method Thereof





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QY 30 GCGCGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
Db 9 GCGCGCAGGCTTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCTGAATTC A 66
QY 90 GAGCNGCCGAGCGGGTGAATATACTATTAGGAATCTAAGTGTAGTGGGGGATAGCTCGGG 149
Db 67 G---CGCGCGAGCGGTGAGTAATGCTTAGGAATCTGCTGTTAGTGGGGGACAACTGCTC 123
QY 150 GAACTCGAATTAATACCCATACGT-CTACGGGAGAAACGACGGGNNCTATTAGACCTTG 208
Db 124 GAAAGGACGCTAATACCCATACGTCTACGGGAGAAACGAGGGACCTTCGGGCGCTTG 183
QY 209 CGCTATTAGATGAGCCTAAGTCGGAATTAGCTAGATGTTGGGTAAAGGCGCTACCATGGCG 268
Db 184 CCCTATCAGATGAGCCTAGTCCGGAATAGCTAGTGGTGAAGTAATGAGCTCACCAGCGG 243
QY 269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCGGA 328
Db 244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTACACTGGAAGTGAAGACAGCGTCCAGA 303
QY 329 CT-CTACGGAGGACAGTGGGGAATATTGGACAATGNGNGGAACCCCTGATCAGCCAT 387
Db 304 CTCCTAGGGAGGACAGTGGGGAATATTGGACAATGNGNGGAACCCCTGATCAGCCAT 363
QY 388 GCCCGCTGTGGAAGAGCCCTTTTGGTTGTAAGACACTTTAGCAGAGTGAAGAGACTCT 447
Db 364 GCCCGCTGTGGAAGAGCTCTCCGGAATGTAAGACACTTTAAGTTGGGAGGAGGCGAT 423
QY 448 TCGGTTAATACCGGGGAGATGACATTAGCTGCAGAAATAGCACCGGCTAACTCTGTGC 507
Db 424 TAACTAATACGTTAGTGTGTTGAGCTTACCGACAGAAATAGCACCGGCTAACTCTGTGC 483
QY 508 CAGCAGCCGGGTAAATACAGAGGTTGCAAGGTTAATCGGAATTAATCTGGGCTAAAGGA 567
Db 484 CAGCAGCCGGGTAAATACAGAGGTTGCAAGGTTAATCGGAATTAATCTGGGCTAAAGGC 543
QY 568 GGGTAGGTGGCTTGAATGTCAGATGTGAATATCCCGGCTTAACTCGGGAAGTGCATCT 627
Db 544 GGGTAGGTGGTTTGTAGTTGATGTGAAGGCTTAACTCGGGAAGTGCATCT 603
QY 628 GAACTGTAGCTAGTGTAGTGTAGAGGGAAGTAGAATTTACAGTGTAGCGGTGAATG 687
Db 604 AAACTGCAAGCTAGAGTATGTTAGAGGTTGTTGGAATTTCTGTGTAGCGGTGAATG 663
QY 688 CBTAGAGTCTGAAGAAATACGATGCGGAGGAGCGCTTCTGGCATCATCTGACATG 747
Db 664 CBTAGATAGGAAGAACACACAGTGGCGAAGGCGACCTGGGACTGATCTGACATG 723
QY 748 AGGCTCGAAAGCGTGGTAGCAACAGAGTATAGTACCTGGTAGTCCACGCGCTAAACG 807
Db 724 AGGCTCGAAAGCGTGGTAGCAACAGAGTATAGTACCTGGTAGTCCACGCGCTAAACG 783
QY 808 ATGTCTACTAGTCTGGGTGCTTGGAGCTTGTAGAGCTTGTAGCAGCAGCTAACCAATAGTAGA 867
Db 784 ATGTCAACTAGCCGTTGGGAGCTTGTAGCTTGTAGTGGCGCAGCTAACCAATAGTAGTA 843
QY 868 CGGCTGGGAGTAGCGCCGCAAGGTTAAACTCAATGAATTCAGCGGGGCGCCGCAAA 927
Db 844 CGGCTGGGAGTAGCGCCGCAAGGTTAAACTCAATGAATTCAGCGGGGCGCCGCAAA 903
QY 928 GGGTGGAGAGTGGTTAATTCGATCAACGGGAAGAACCTTACCTGGTCTTTCACATA 987
Db 904 GGGTGGAGAGTGGTTAATTCGAGCAACGGGAAGAACCTTACCGGCTTTCACATC 963
QY 988 CACAGAATCTTTAGAGATACGAGATGCTCTTCGGAATTTGTGATACAGGTGCTGCATGG 1047
Db 964 CAATGAATCTTTCCAGAGATGGTGGTGGCTTCGGAACATTTGAGACAGGTGCTGCATGG 1023
QY 1048 CTGTGCTCAGCTCTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTGT 1107
Db 1024 CTGTGCTCAGCTCTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTGT 1083
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QY 1108 CTTTAGTTACAGCAC-TTCGGTGGGAACCTCTAAGGATACCTCCAGTGCACAACTGGAG 1166
Db 1084 CTTTAGTTACAGCACGTAATGTTGGGCACCTCTAAGGAGACTGCCGTTGCACAAACCGGAG 1143
QY 1167 GAAGCGGGGACAGAGCTCAAGTCAATCATGGCCCTTAGCACCAGGCTACACACGTGCTAC 1226
Db 1144 GAAGTGGGATGACGTCAAGTCAATCATGGCCCTTAGCACCAGGCTACACACGTGCTAC 1203
QY 1227 AATGTAGTACAGAGGCGAGCTACACAGCGATCTGATCGAATCTCAAAAAGCCTATCG 1286
Db 1204 AATGTCTGTACAGAGGTTGCCAAGCCGAGGTGAGCTAATCCCAAAACCGATCG 1263
QY 1287 TAGTCCAGATTGGAGTCTGCACTCGACTTCCAACTAGGAATAGGAATCTAGTAAATCGCGA 1346
Db 1264 TAGTCCGATCGAGTCTGCACTCGACTCGAGTGAATCGGAATCTAGTAAATCGGAA 1323
QY 1347 TCAGAATCCCGGTGAATACGTTCCCGGCTTGTACACACCGCCCTCACCACATGGG 1406
Db 1324 TCAGAATCTCCGCTGAATACGTTCCCGGCTTGTACACACCGCCCTCACCACATGGG 1383
QY 1407 AGTTGATTGCACAGAGTGGTTAGCCTAA-CTTAGTGAGGCGGATCACCAGGTGTGCT 1465
Db 1384 AGTGGTTGCAACAGAGTAGTCTAGTCTAATCTTCGGGAGGAGCGGTACCGGTTGTAT 1443
QY 1466 CGATGACTGGGTTGAAGTCTGTAACAGAGTAGCCGTAGGGGAACCTCGGCTGGATCAC 1523
Db 1444 TCATGACTGGGTTGAAGTCTGTAACAGAGTAGCCGTAGGGGAACCTCGGCTGGATCAC 1501
```

RESULT 8  
US-10-218-519-5  
; Sequence 5, Application US/10218519  
; Publication No. US20030049806A1  
; GENERAL INFORMATION:  
; APPLICANT: Yano, Takeshi  
; APPLICANT: Imamura, Takeshi  
; APPLICANT: Suda, Sakae  
; APPLICANT: Honma, Tsutomu  
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthese and Gene Encoding the Same Enzy  
; FILE REFERENCE: 03500.015225.1  
; CURRENT APPLICATION NUMBER: US/10/218,519  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/821,016  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 5  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii Pl61 ; BP-7376  
; FEATURE: cdna to 16S rRNA  
US-10-218-519-5

Query Match 72.0% ; Score 1098.6 ; DB 14 ; Length 1501 ;  
Best Local Similarity 85.9% ; Pred. No. 2.3e-289 ;  
Matches 1287 ; Conservative 0 ; Mismatches 202 ; Indels 9 ; Gaps 6 ;

QY 30 GCGCGCAGGCTTAACACATGCAAGTGCAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89  
Db 9 GCGCGCAGGCTTAACACATGCAAGTGCAGCGG--ATGACGGGAGCTTGCTCTGAATTC A 66  
QY 90 GAGCNGCCGAGCGGTGAGTAATTAATCCGATACGT-CTACGGGAGAAACGACGGGNNCTATTAGACCTTG 208  
Db 67 G---CGCGCGAGCGGTGAGTAATGCTTAGGAATCTGCTGTTAGTGGGGGACAACTGCTC 123  
QY 150 GAACTCGAATTAATACCCATACGT-CTACGGGAGAAACGACGGGNNCTATTAGACCTTG 208  
Db 124 GAAAGGACGCTAATACCCATACGTCTACGGGAGAAACGAGGGACCTTCGGGCGCTTG 183  
QY 209 CGCTATTAGATGAGCCTAAGTCGGAATTAGCTAGATGTTGGGTAAAGGCGCTACCATGGCG 268  
Db 184 CCCTATCAGATGAGCCTAGTCCGGAATAGCTAGTGGTGAAGTAATGAGCTCACCAGCGG 243





QY 508 CAGCAGCGCGGTAATACACAGCGGTCCRAAGCGTTAAATCGGAATTACTGGCGGTAAGCGA 567  
Db 484 CAGCAGCGCGGTAATACACAGCGGTCCRAAGCGTTAAATCGGAATTACTGGCGGTAAGCGC 543  
QY 568 GCGTAGGTGGCTTGAATAGTCAGATGTAATATCCCGGGCTTAACCTGGGAACTGCATCT 627  
Db 544 GCGTAGGTGGCTTGAATAGTCAGATGTAATATCCCGGGCTTAACCTGGGAACTGCATCT 603  
QY 628 GAACTGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGT 687  
Db 604 AAACTGCAAGCTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAG 663  
QY 688 CCGTAGAGTCTGAGAGGATACGATCGCGAGGCGAGCTTCTGGCATCATATGACATCG 747  
Db 664 CCGTAGATATAGGAGGAGAACCCAGTGGCGAGGCGAGCTTCTGGCATCATATGACATCG 723  
QY 748 AGGCTCGAAAGCGTGGGTAGCAAAACAGAGATTAGATACCTGGTAGTCCAGCGCGTAAACG 807  
Db 724 AGGTGCGAAGCGTGGGAGCGACACAGAGATTAGATACCTGGTAGTCCAGCGCGTAAACG 783  
QY 808 ATGTCTACTAGTCTGGTCCCTGTGAGGACTTGTAGCGAGCTTAACCGCAATAAGTAGA 867  
Db 784 ATGTCAACTAGTCTGGGAGCGCTTGTAGCTCTTAGTGGCGAGCTTAACCGCAATAAGTAGA 843  
QY 868 CCGCTTGGGAGTACGCGCCGACAGGTTAAATCTCAATTAATTCAGCGGGGCCGACAA 927  
Db 844 CCGCTTGGGAGTACGCGCCGACAGGTTAAATCTCAATTAATTCAGCGGGGCCGACAA 903  
QY 928 GCGGTGGAGCATGTGGTTAAATTCGATGCAACGCGAGAACCTTACTGTGTGTGACATA 987  
Db 904 GCGGTGGAGCATGTGGTTAAATTCGAGCAACGCGAGAACCTTACCAGGCTTGACATC 963  
QY 988 CACAGAACTTGTAGACATAGAGAGTGCCTTCGCGGAATGTGTACAGGTGCTGCATGG 1047  
Db 964 CAATGAACCTTCCAGAGATGGATGGTGGCTTCGCGGAATGTGTACAGGTGCTGCATGG 1023  
QY 1048 CTGTCTCAGTCTGTGCTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCTTGT 1107  
Db 1024 CTGTCTCAGTCTGTGCTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCTTGT 1083  
QY 1108 CTTTATGTTACCAAGCAC-TTCGGGTGGGAATCTTAAGTATCTGCCAGTGCACAACTGGAG 1166  
Db 1084 CTTTATGTTACCAAGCACGTAATGTTGGGCACCTCTAAGGAGACTGCGGCTGACAAACCGGAG 1143  
QY 1167 GAAGCGGGGAGCAGCTCAAGTCAATGCGCCCTTACGACAGGGCTACACAGCTGCTAC 1226  
Db 1144 GAAGTGGGGATGACGTCAGTCAATGCGCCCTTACGCGCTTGGGCTACACAGCTGCTAC 1203  
QY 1227 AATGTTAGTACAGAGGCGAGCTACACAGGATGTGATGCGAATCTCAAAAAGCCTATCG 1286  
Db 1204 AATGTTAGTACAGAGGTTGCCAAGCGGAGGTGGAGCTAATCCCAACAAACCGATCG 1263  
QY 1287 TAGTCCAGATTGGAGTCTGCAACTCGACTTCCATGAAGTAGGAATFCGTAGTAAATCGCGGA 1346  
Db 1264 TAGTCCGATGCGAGTCTGCAACTCGACTGCGTGAAGTCGGAATFCGTAGTAAATCGCGGA 1323  
QY 1347 TCAGATGCGCGGTGTAATAGTTCGCGGCCCTTGTACACACCGCGCGTACACCATGGG 1406  
Db 1324 TCAGATGTCGCGGTGTAATAGTTCGCGGCCCTTGTACACACCGCGCGTACACCATGGG 1383  
QY 1407 AGTGTATGTCACAGAGAGTGGTTAGGCTAA-CTTAGTGGGCGGATCACACCGGTGTGTGT 1465  
Db 1384 AGTGGTTGCACAGAGAGTGTAGTCTAATCTCGGAGGACGGTTACACCGGTGTGTGT 1443  
QY 1466 CGATGACTGGGTGAGTCTGCAATGCAAGGTAGCGGTAGGGAGACCTGCGGTGGATCAC 1523  
Db 1444 TCATGACTGGGTGAGTCTGCAATGCAAGGTAGCGGTAGGGAGACCTGCGGTGGATCAC 1501

RESULT 10

US-10-252-518-5

; Sequence 5, Application US/10252518

; Publication No. US20030087413A1

; GENERAL INFORMATION:

; APPLICANT: Iano, Tetsuya

; APPLICANT: Imamura, Takeshi

; APPLICANT: Suda, Sakae

; APPLICANT: Honma, Tsutomu

; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enz

; CURRENT APPLICATION NUMBER: US/10/252,518

; PRIOR FILING DATE: 2002-09-24

; PRIOR APPLICATION NUMBER: JP 2000-095004

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: Microsoft Word

; SEQ ID NO 5

; LENGTH: 1501

; TYPE: DNA

; ORGANISM: Pseudomonas jessenii P161 ; BP-7376

; FEATURE:

; FEATURE: cDNA to 16S rRNA

US-10-252-518-5

Query Match

Best Local Similarity 72.08; Score 1098.6; DB 14; Length 1501;

Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

QY 30 GCGGCGAGGCTTACACATCATGTCGAGCGGAAACGATGATAGCTTGTATTAGCGCTC 89

Db 9 GCGGCGAGGCTTACACATCATGTCGAGCGG--ATGACGGGAGCTTGTCTCTGAATTCA 66

QY 90 GAGCNCGCGGAGCGGTGAGTAATTAATCTAGGAATCTACCTAGTCTAGTGGGAGATACGCGG 149

Db 67 G---CGCGGAGCGGTGAGTAATTAATCTAGGAATCTCTCTAGTGGGAGATACGCTC 123

QY 150 GAACTCTGAATTAATACCGCATAGCT-CTACGGGAGAAAGCAGGGGNTCAATAGACCTTG 208

Db 124 GAAAGGAGCGCTTAATACCGCATAGCTCTACGGGAGAAAGCAGGGGACCTTCGGGCGCTG 183

QY 209 CGCTATAGTAGAGCCTTAAGTCGAGATTAGTAGTGGGTAAAGGCTAACGCTACATGGCG 268

Db 184 CGCTATAGTAGAGCCTTAAGTCGAGATTAGTAGTGGGTAAAGGCTAACGCTACATGGCG 243

QY 269 ACATCTGTAGTGTCTGTGAGGAGATGATCAGCCACACCGGAGCTGAGACACGGCCCGGA 328

Db 244 ACATCTGTAGTGTCTGTGAGGAGATGATCAGCCACACCGGAGCTGAGACACGGCCCGGA 303

QY 329 CT-CTACGGGAGGACAGTAGTGGGGAATATTGGAATATGNGGGAACCTGATCCAGCAT 387

Db 304 CTCTACGGGAGGACAGTAGTGGGGAATATTGGAATATGNGGGAACCTGATCCAGCAT 363

QY 388 GCGCGTGTGTGAAGAGCGCTTTTGGTTGAAAGCATTAAAGCAGTGAAGAGACTCT 447

Db 364 GCGCGTGTGTGAAGAGCGCTTTTGGTTGAAAGCATTAAAGCAGTGAAGAGACTCT 423

QY 448 TCGGTTAATPACCCGGGAGCAGTACATTAAGTCTGAGAAATAAGCACCAGCTTCTGTC 507

Db 424 TAACCTAATACCTTGTAGTCTTTTGGCTTACCGACAGATAAGCACCAGCTTCTGTC 483

QY 508 CAGCAGCGCGGTAAATACAGAGGTCGAGAGGTGAGAGGTGAGAGGTGAGAGGTGAGAGGT 567

Db 484 CAGCAGCGCGGTAAATACAGAGGTCGAGAGGTGAGAGGTGAGAGGTGAGAGGTGAGAGGT 543

QY 568 GCGTAGGTGGCTTGAATAGTCAGATGTGAAATCCCGGGCTTAACCTGGGAACTGCATCT 627

Db 544 GCGTAGGTGGCTTGAATAGTCAGATGTGAAATCCCGGGCTTAACCTGGGAACTGCATCT 603

QY 628 GAAACTGTTTAGCTAGAGTGTGAGAGGAAAGTGAATTTTCAAGTGTAGCGTGAATG 687

Db 504 ARAACTGACACAGTGTAGATGTTAGAGGTTGTTGGAATTTTCTGTGTAGCGTGAATG 663

QY 688 CGTAGAGTCTGAAGGAATACCGGATGCGGAGGAGCTTCTCTGCATCATATGACATG 747

Db 664 CGTAGATATAGGAGGAACACCACTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 723







QY 1465 TCGATGACTGGGGTGAAGTCGTAAACAAGGTA 1495  
DB 1464 TCGATGACTGGGGTGAAGTCGTAAACAAGGTA 1494

## RESULT 14

US-09-737-297-4

; Sequence 4, Application US/09737297

; Patent No. US20020072108A1

; GENERAL INFORMATION:

; APPLICANT: Berry, Mark

; APPLICANT: Griffiths, Allen

; APPLICANT: Hill, Philip

; APPLICANT: Laybourne-Parry, Johanna

; APPLICANT: Mills, Sarah

; TITLE OF INVENTION: Processes and Organisms for the Production of Antifreeze Proteins

; FILE REFERENCE: F3247

; CURRENT APPLICATION NUMBER: US/09/737,297

; CURRENT FILING DATE: 2000-12-15

; PRIOR APPLICATION NUMBER: GB 9929696.4

; PRIOR FILING DATE: 1999-12-15

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4

; LENGTH: 1481

; TYPE: DNA

; ORGANISM: Marinomonas communis

; FEATURE:

; NAME/KEY: Unsure

; LOCATION: (1)..(1)

; OTHER INFORMATION: base identity unsure

; NAME/KEY: Unsure

; LOCATION: (203)..(204)

; OTHER INFORMATION: base identity unsure

; NAME/KEY: Unsure

; LOCATION: (840)..(840)

; OTHER INFORMATION: base identity unsure

; NAME/KEY: Unsure

; LOCATION: (964)..(965)

; OTHER INFORMATION: base identity unsure

; NAME/KEY: Unsure

; LOCATION: (1142)..(1142)

; OTHER INFORMATION: base identity unsure

; NAME/KEY: Unsure

; LOCATION: (1182)..(1182)

; OTHER INFORMATION: base identity unsure

; NAME/KEY: Unsure

; LOCATION: (1185)..(1186)

; OTHER INFORMATION: base identity unsure

; NAME/KEY: Unsure

; LOCATION: (1449)..(1449)

; OTHER INFORMATION: base identity unsure

US-09-737-297-4

Query Match 70.4%; Score 1073.8; DB 9; Length 1481;  
Best Local Similarity 86.0%; Pred. No. 1.3e-282;  
Matches 1242; Conservative 0; Mismatches 198; Indels 5; Gaps 5;

QY 30 GCGCGCAGCTTACACATGCAAGTCGAGCGGAACGATGATGCTGCTATTAGCGGTC 89  
DB 39 GCGCGCAGCTTACACATGCAAGTCGAGCGGTAACATGCTAGCTTGTAGAAATGAC 98

QY 90 GAGCNCGCGAGCGGTGAGTAATCTAGGAATCTACCTAGTGTGGGGATAGCTCGG 149  
DB 99 GAGCGG-CGAGCGGGTGAAGTAAACCGCTAGGAATCTGCCTAGTGTGGGGACACATG 157

QY 150 GAAACPCGAATTAATPACCGATAGC-TCTACGGGGAAGACGAGGNNICATTAGACTTG 208  
DB 158 GAAACCGATGCTAATPACCGATAGCCTACGCGGGAAGAGGAGGNNICTTCGACCTTT 217

QY 209 CGCTATTAGATGAGCTTAAGTCGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 268  
DB 218 CGCTATTAGATGAGCTTACGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 277



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QY 1348 CAGAAATCCCGGCTGAATACGTTCCCGGCTTGTACACACGCCCGCTCACACCATGGGA 1407
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Db 1357 CAGAAATCCCGGCTGAATACGTTCCCGGCTTGTACACACGCCCGCTCACACCATGGGA 1416
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1408 GTTGATTCACACCAAGTGGTTAGCTTAA-CTTAGTGAGGCGATCACACGTTGGTC 1466
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1417 GTTGATTCACACCAAGTGGTTAGCTTAA-CTTAGTGAGGCGATCACACGTTGGTC 1476
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1467 GATGA 1471
      |||||
Db 1477 AATGA 1481
      |||||

RESULT 15
US-09-726-774-3
; Sequence 3, Application US/09726774
; Patent No. US20020082226A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-726-774-3

Query Match 70.2%; Score 1070.8; DB 9; Length 1467;
Best Local Similarity 85.9%; Pred. No. 8.8e-282;
Matches 1233; Conservative 0; Mismatches 199; Indels 4; Gaps 4;

QY 95 GCCGGACGGTGGATTAATCTAGGAATCTACCTAGTAGTGGGGATAGCTCGGGAAAC 154
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 29 GCCGGACGGTGGATTAATCTAGGAATCTAGGAATCTAGTGGGGACACACCTTCGAAG 88
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 155 TCGAATTAATACCGCATAGCT-CTACGGGAGAAAGCAGGGGNNPCTATTAGCTTCCGCTA 213
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 89 CAACGCTAATACCGCATAGCTCTACGGGAGAAAGCAGGGGACCTTCGGGCTTCGCTA 148
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 214 TTAGTACGCTTAAGTCGATAGCTAGTGGGGTAAAGCCCTACCTAGCTGGGACGAT 273
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 149 TCAGATGAGCTTAGTGGGATAGCTAGTGGGATAGCTAGCTACCAAGGCGGAT 208
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 274 CTGTAGCTGTCTGAGAGATGATCAGCCACACCGGACTGAGACACGGCCCGGACT-CT 332
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 209 CCGTAATCTGTCTGAGAGATGATCAGTCACACTGGACTGAGACAGGTCAGACTCCT 268
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 333 ACCGGAGCAGCAGTGGGGAATPAGCAATGNGNGGAACCCCTGATCCAGCCATGCCG 392
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Db 269 ACCGGAGCAGCAGTGGGGAATPAGCAATGNGNGGAACCCCTGATCCAGCCATGCCG 328
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QY 573 GGTGGCTTGATAGTCAGATGTGAATCCCGGCTTAACCTGGGAACTGATCTGAAC 632
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Search completed: August 20, 2003, 06:42:13  
Job time : 1528.06 secs

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QY 753 CGAAAGCGTGGTGGTACCAACAGGATAGATACCTCGTGTAGTCCAGCCGTAAGAGTTC 812
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Db 989 GTCAGCTCGTCTCGTGAGATGTTGGTTAAAGTCCCGTAAAGAGCGCAACCCCTTCCTTA 1048
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QY 1292 CAGATTGGAGTCTGCAACTCGACTCCATGAATAGGAATCGCTAGTAAATCGCGATCAGA 1351
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Db 1229 CGGATCGCAGTCTGCAACTCGACTCGGTGAAGTCGGAAATCGCTAGTAAATCGGAATCAGA 1288
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QY 1352 ATGCCGGGTGAATAGCTTCCCGGGCTTGTACACACCGCCGCTCACACCATGGGAGTTG 1411
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 00:33:30 ; Search time 71.3884 Seconds  
(without alignments)  
10888.092 Million cell updates/sec

Title: US-09-979-558a-2

Perfect score: 19

Sequence: 1 taatgtcatcgtcccccgg 19

Scoring table: IDENTITY\_NOC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

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27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rod.\*

36: em\_htg\_mam.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	19	100.0	19	6	E58428	E58428 DNA probe f
2	19	100.0	300	1	AF025555	AF025555 Psychroba
3	19	100.0	1403	1	AB094456	AB094456 Psychroba
4	19	100.0	1462	1	AB094458	AB094458 Psychroba
5	19	100.0	1520	1	AB016059	AB016059 Psychroba
6	19	100.0	1525	1	AB016056	AB016056 Psychroba
7	19	100.0	1526	1	AB016057	AB016057 Psychroba
8	19	100.0	1526	6	E58427	E58427 DNA probe f
9	19	100.0	1530	1	AB016058	AB016058 Psychroba
10	19	100.0	1531	1	AB016055	AB016055 Psychroba
11	19	100.0	1536	1	AB016054	AB016054 Psychroba
12	17.4	91.6	161	1	AF440839	AF440839 Unculture
13	17.4	91.6	165	1	AF440847	AF440847 Unculture
14	17.4	91.6	168	1	AF440851	AF440851 Unculture
15	17.4	91.6	170	1	AF440834	AF440834 Unculture
16	17.4	91.6	170	1	AF440837	AF440837 Unculture
17	17.4	91.6	171	1	AF440838	AF440838 Unculture
18	17.4	91.6	172	1	AF128774	AF128774 Unculture
19	17.4	91.6	172	1	AF440831	AF440831 Unculture
20	17.4	91.6	174	1	AF440842	AF440842 Unculture
21	17.4	91.6	175	1	AF440832	AF440832 Unculture
22	17.4	91.6	175	1	AF440846	AF440846 Unculture
23	17.4	91.6	177	1	AF128777	AF128777 Unculture
24	17.4	91.6	691	1	AY159801	AY159801 Psychroba
25	17.4	91.6	692	1	AY159792	AY159792 Psychroba
26	17.4	91.6	700	1	PSP244767	PSP244767 Psychroba
27	17.4	91.6	717	1	PSP244768	PSP244768 Psychroba
28	17.4	91.6	880	1	AF513419	AF513419 Psychroba
29	17.4	91.6	1354	1	AF505742	AF505742 Bacterium
30	17.4	91.6	1401	1	AF505736	AF505736 Bacterium
31	17.4	91.6	1409	1	PSU85874	PSU85874 Psychrobact
32	17.4	91.6	1425	1	AF505724	AF505724 gamma pro
33	17.4	91.6	1425	1	AF505739	AF505739 Bacterium
34	17.4	91.6	1426	1	PSP272303	PSP272303 Psychroba
35	17.4	91.6	1441	1	AY165598	AY165598 Unculture
36	17.4	91.6	1441	1	PGU85878	PGU85878 Psychrobact
37	17.4	91.6	1445	1	AF468383	AF468383 Arctic se
38	17.4	91.6	1445	1	PIU85880	PIU85880 Psychrobact
39	17.4	91.6	1449	1	AY165583	AY165583 Unculture
40	17.4	91.6	1457	1	AF468390	AF468390 Arctic se
41	17.4	91.6	1458	1	PGL539102	PGL539102 Psychroba
42	17.4	91.6	1459	1	AY167310	AY167310 Psychroba
43	17.4	91.6	1460	1	AF170743	AF170743 Psychroba
44	17.4	91.6	1460	1	AF170747	AF170747 Psychroba
45	17.4	91.6	1462	1	PGU85877	PGU85877 Psychrobact

ALIGNMENTS

RESULT 1  
E58428  
LOCUS E58428 19 bp DNA linear PAT 31-JAN-2002  
DEFINITION DNA probe for detecting novel psychrophile.  
ACCESSION E58428  
VERSION E58428.1 GI:18622290  
KEYWORDS JP 2000333680-A/2.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Maruyama,A., Kitamura,K. and Kurane,R.  
TITLE DNA probe for detecting novel psychrophile  
JOURNAL Patent: JP 2000333680-A 2 05-DEC-2000;  
AGENCY OF IND SCIENCE & TECHNOL

```

COMMENT      OS      Artificial Sequence
PN      JP      2000333680-A/2
PD      05-DEC-2000
PF      25-MAY-1999      JP      1999145342
PR
PI      AKIHIKO MARYAMA, KEIKO KITAMURA, RYUICHIRO KURANE
C12N15/09, C12N1/20, C12G1/68//C12N15/09, C12R1/01, (C12N1/20, PC
C12R1/01),
PC      C12N15/00, (C12N15/00, C12R1/01)
CC
FH      Key      Location/Qualifiers
FT      1. .19      /organism='Artificial Sequence'
FEATURES
source      Location/Qualifiers
1. .19
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
3 a      6 c      5 g      5 t
BASE COUNT      3 a      6 c      5 g      5 t
ORIGIN
Query Match      100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TAATGTCATGTCCTCCGGG 19
Db      1 TAATGTCATGTCCTCCGGG 19
RESULT 2
AF025555/c
LOCUS      300 bp      DNA      linear      BCT 11-SEP-2000
DEFINITION      Psychrobacter glacincola 16S ribosomal RNA gene, partial sequence.
ACCESSION      AF025555
VERSION      AF025555.1      GI:2582456
KEYWORDS
SOURCE      Psychrobacter glacincola
ORGANISM      Psychrobacter glacincola
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.
REFERENCE      1 (bases 1 to 300)
Hagstrom, A., Pinhassi, J. and Zweifel, U.L.
Biogeographical diversity among marine bacterioplankton
Aquat. Microb. Ecol. 21, 231-244 (2000)
2 (bases 1 to 300)
Pinhassi, J., Zweifel, U.L. and Hagstrom, A.
Direct Submission
Submitted (18-SEP-1997) National Environmental Research Institute,
Frederiksborgvej 399, Roskilde DK-4000, Denmark
Location/Qualifiers
1. .300
/organism='Psychrobacter glacincola'
/mol_type='genomic DNA'
/db_xref='taxon:56810'
/notes='isolated from the NW Mediterranean'
<1. >300
rRNA      /product='16S ribosomal RNA'
77 a      66 c      95 g      62 t
BASE COUNT      77 a      66 c      95 g      62 t
ORIGIN
Query Match      100.0%; Score 19; DB 1; Length 300;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TAATGTCATGTCCTCCGGG 19
Db      268 TAATGTCATGTCCTCCGGG 250
RESULT 3
AB094456/c

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LOCUS      AB094456      1403 bp      DNA      linear      BCT 16-JAN-2003
DEFINITION      Psychrobacter sp. MJYP.15.12 gene for 16S rRNA, partial sequence.
ACCESSION      AB094456
VERSION      AB094456.1      GI:27807566
KEYWORDS
SOURCE      Psychrobacter sp. MJYP.15.12
ORGANISM      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.
REFERENCE      1
Inagaki, F., Suzuki, M., Takai, K. and Horikoshi, K.
Microbial community structure in subseafloor sediments from the Sea
of Okhotsk
Published Only in Database (2003)
2 (bases 1 to 1403)
Direct Submission
Inagaki, F.
Submitted (23-OCT-2002) Fumio Inagaki, Japan Marine Science &
Technology Center, Subground Animalcule Retrieval (SUGAR) Project,
Frontier Research System for Extremophiles; Natsuchina-cho 2-15,
Yokosuka 237-0061, Japan (E-mail: inagaki@jamstec.go.jp,
Tel:81-468-67-9687, Fax:81-468-67-9715)
Location/Qualifiers
1. .1403
/organism='Psychrobacter sp. MJYP.15.12'
/mol_type='genomic DNA'
/strain='MJYP.15.12'
/isolation_source='subseafloor sediment'
/db_xref='taxon:211898'
<1. >1403
rRNA      /product='16S ribosomal RNA'
375 a      308 c      427 g      293 t
BASE COUNT      375 a      308 c      427 g      293 t
ORIGIN
Query Match      100.0%; Score 19; DB 1; Length 1403;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TAATGTCATGTCCTCCGGG 19
Db      458 TAATGTCATGTCCTCCGGG 440
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AB094458/c
LOCUS      AB094458      1462 bp      DNA      linear      BCT 16-JAN-2003
DEFINITION      Psychrobacter sp. MJYP.25.32 gene for 16S rRNA, partial sequence.
ACCESSION      AB094458
VERSION      AB094458.1      GI:27807568
KEYWORDS
SOURCE      Psychrobacter sp. MJYP.25.32
ORGANISM      Psychrobacter sp. MJYP.25.32
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.
REFERENCE      1
Inagaki, F., Suzuki, M., Takai, K. and Horikoshi, K.
Microbial community structure in subseafloor sediments from the Sea
of Okhotsk
Published Only in Database (2003)
2 (bases 1 to 1462)
Direct Submission
Inagaki, F.
Submitted (23-OCT-2002) Fumio Inagaki, Japan Marine Science &
Technology Center, Subground Animalcule Retrieval (SUGAR) Project,
Frontier Research System for Extremophiles; Natsuchina-cho 2-15,
Yokosuka 237-0061, Japan (E-mail: inagaki@jamstec.go.jp,
Tel:81-468-67-9687, Fax:81-468-67-9715)
Location/Qualifiers
1. .1462
/organism='Psychrobacter sp. MJYP.25.32'
/mol_type='genomic DNA'
/strain='MJYP.25.32'
/isolation_source='subseafloor sediment'

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/db_xref="taxon:211899"
<1..>1462
/product="16S ribosomal RNA"
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ORIGIN
Query Match      100.0%; Score 19; DB 1; Length 1462;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TAATGTCATCGTCCCGGG 19
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Db      456 TAATGTCATCGTCCCGGG 438

RESULT 5
AB016059/c
LOCUS      AB016059          1520 bp    DNA         linear     BCT 10-MAY-2000
DEFINITION Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
            strain:NIBH P2K18.
ACCESSION      AB016059
VERSION        1 GI:5691640
KEYWORDS       16S ribosomal RNA.
SOURCE         Psychrobacter pacificensis
ORGANISM       Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
            Moraxellaceae; Psychrobacter.
REFERENCE      1 (sites)
AUTHORS        Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.
TITLE          Phylogenetic analysis of psychrophilic bacteria isolated from the
            Japan Trench, including a description of the deep-sea species
            Psychrobacter pacificensis sp. nov
JOURNAL        Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
MEDLINE        20222194
PUBMED        10758895
FEATURES             source
                     Location/Qualifiers
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                             /mol_type="genomic DNA"
                             /strain="NIBH P2J13"
rRNA              <1..>1525
                    /db_xref="taxon:112002"
BASE COUNT      398 a   334 c   468 g   325 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TAATGTCATCGTCCCGGG 19
        |||
Db      473 TAATGTCATCGTCCCGGG 455

RESULT 7
AB016057/c
LOCUS      AB016057          1526 bp    DNA         linear     BCT 10-MAY-2000
DEFINITION Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
            strain:NIBH P2K6(T)(=IFO 16279(T)).
ACCESSION      AB016057
VERSION        1 GI:6691638
KEYWORDS       16S ribosomal RNA.
SOURCE         Psychrobacter pacificensis
ORGANISM       Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
            Moraxellaceae; Psychrobacter.
REFERENCE      1 (sites)
AUTHORS        Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.
TITLE          Phylogenetic analysis of psychrophilic bacteria isolated from the
            Japan Trench, including a description of the deep-sea species
            Psychrobacter pacificensis sp. nov
JOURNAL        Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
MEDLINE        20222194
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rRNA              <1..>1526
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AUTHORS	Maruyama, A., Honda, D., Yanamoto, H., Kitamura, K. and Higashihara, T.
TITLE	Phylogenetic analysis of psychrophilic bacteria isolated from the Japan Trench, including a description of the deep-sea species
ABSTRACT	
KEYWORDS	
QUERY MATCH	100.0%; Score 19; DB 1; Length 1531;
BEST LOCAL SIMILARITY	100.0%; Pred. No. 39;

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAATGTCATCGTCCCGGG 19
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Db 484 TAATGTCATCGTCCCGGG 466

RESULT 11
AB016054/c
LOCUS      1536 bp      DNA      linear      BCT 10-MAY-2000
DEFINITION Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
            strain.NIBH P2J2.
ACCESSION AB016054
VERSION   AB016054.1 GI:6691635
KEYWORDS  16S ribosomal RNA.
SOURCE    Psychrobacter pacificensis
ORGANISM  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
            Moraxellaceae; Psychrobacter.
REFERENCE 1 (sites)
AUTHORS   Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.
TITLE     Phylogenetic analysis of psychrophilic bacteria isolated from the
            Japan Trench, including a description of the deep-sea species
            Psychrobacter pacificensis sp. nov
JOURNAL   Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
MEDLINE   20222134
PUBMED    10758895
REFERENCE 2 (bases 1 to 1536)
AUTHORS   Maruyama,A. and Kitamura,K.
TITLE     Direct Submission
JOURNAL   Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
            Bioscience and Human-Technology, Department of Applied and
            Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
            Japan (E-mail:maruyama@nibh.go.jp, Tel:+81-298-54-6062,
            Fax:+81-298-54-6412)
FEATURES   Location/Qualifiers
            source
                1..1536
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                /strain="NIBH P2J2"
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                /product="16S ribosomal RNA"
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                405 a 335 c 472 g 324 t
BASE COUNT 405 a 335 c 472 g 324 t
ORIGIN
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    Best Local Similarity 100.0%; Pred. No. 39;
    Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAATGTCATCGTCCCGGG 19
    |||||
Db 476 TAATGTCATCGTCCCGGG 458

RESULT 12
AF440839/c
LOCUS      161 bp      DNA      linear      BCT 25-NOV-2001
DEFINITION Uncultured gamma proteobacterium 16S ribosomal RNA gene, partial
            sequence.
ACCESSION AF440839
VERSION   AF440839.1 GI:17064094
KEYWORDS  uncultured gamma proteobacterium
SOURCE    uncultured gamma proteobacterium
ORGANISM  Bacteria; Proteobacteria; Gammaproteobacteria; environmental
            samples.
            1 (bases 1 to 161)
REFERENCE 1
AUTHORS   Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE     Bioremediation Treatment Effects On Microbial Community Structure
            In A Crude Oil-Contaminated Coastal Marsh
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 161)
AUTHORS   Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE     Direct Submission
JOURNAL   Submitted (30-OCT-2001) Civil and Environmental Engineering,
            University of Cincinnati, 701 ERC, Cincinnati, OH 45221, USA
FEATURES   Location/Qualifiers
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                field study conducted at a coastal marsh"
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BASE COUNT 47 a 34 c 50 g 34 t
ORIGIN
    Query Match 91.6%; Score 17.4; DB 1; Length 165;
    Best Local Similarity 94.7%; Pred. No. 2.8e+02;
    Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TAATGTCATCGTCCCGGG 19
    |||||
Db 147 TAATGTCATCGTCCCGGG 129

RESULT 13
AF440847/c
LOCUS      165 bp      DNA      linear      BCT 25-NOV-2001
DEFINITION Uncultured gamma proteobacterium DGGE band ns.st8.d3-II 16S
            ribosomal RNA gene, partial sequence.
ACCESSION AF440847
VERSION   AF440847.1 GI:17064102
KEYWORDS  uncultured gamma proteobacterium
SOURCE    uncultured gamma proteobacterium
ORGANISM  Bacteria; Proteobacteria; Gammaproteobacteria; environmental
            samples.
            1 (bases 1 to 165)
REFERENCE 1
AUTHORS   Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE     Bioremediation Treatment Effects On Microbial Community Structure
            In A Crude Oil-Contaminated Coastal Marsh
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 165)
AUTHORS   Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE     Direct Submission
JOURNAL   Submitted (30-OCT-2001) Civil and Environmental Engineering,
            University of Cincinnati, 701 ERC, Cincinnati, OH 45221, USA
FEATURES   Location/Qualifiers
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                /country="Canada: Nova Scotia"
                /note="oiled, nutrient-amended plots with existent plants
                (phytoremediation treatment) in an oil bioremediation
                field study conducted at a coastal marsh"
            rRNA
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                /product="16S ribosomal RNA"
BASE COUNT 47 a 34 c 50 g 34 t
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    Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TAATGTCATCGTCCCGGG 19
    |||||
Db 147 TAATGTCATCGTCCCGGG 129

RESULT 14
AF440851/c
LOCUS      168 bp      DNA      linear      BCT 25-NOV-2001

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DEFINITION Uncultured gamma proteobacterium DGGE band ns.st8.e3 16S ribosomal
RNA gene, partial sequence.
ACCESSION AF440834
VERSION AF440834.1 GI:17064106
KEYWORDS
SOURCE uncultured gamma proteobacterium
ORGANISM uncultured gamma proteobacterium
Bacteria; Proteobacteria; Gammaproteobacteria; environmental
samples.
REFERENCE 1 (bases 1 to 168)
AUTHORS Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE Bioremediation Treatment Effects On Microbial Community Structure
In A Crude Oil-Contaminated Coastal Marsh
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 168)
AUTHORS Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-2001) Civil and Environmental Engineering,
University of Cincinnati, 701 ERC, Cincinnati, OH 45221, USA
FEATURES
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/country="Canada; Novia Scotia"
/note="oiled, nutrient-amended plots with plants cut
(bioremediation treatment) in an oil bioremediation field
study conducted at a coastal marsh"
<1..>168
rRNA /product="16S ribosomal RNA"
BASE COUNT 47 a 35 c 51 g 35 t
ORIGIN

Query Match 91.6%; Score 17.4; DB 1; Length 168;
Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TAATGTCATCGTCCCGGG 19
Db |||||||||||
147 TAATGTCATCGTCCCGGG 129

RESULT 15
AF440834/C
LOCUS
DEFINITION Uncultured gamma proteobacterium DGGE band ns.st8.b1 16S ribosomal
RNA gene, partial sequence.
ACCESSION AF440834
VERSION AF440834.1 GI:17064089
KEYWORDS
SOURCE uncultured gamma proteobacterium
ORGANISM uncultured gamma proteobacterium
Bacteria; Proteobacteria; Gammaproteobacteria; environmental
samples.
REFERENCE 1 (bases 1 to 170)
AUTHORS Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE Bioremediation Treatment Effects On Microbial Community Structure
In A Crude Oil-Contaminated Coastal Marsh
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 170)
AUTHORS Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-2001) Civil and Environmental Engineering,
University of Cincinnati, 701 ERC, Cincinnati, OH 45221, USA
FEATURES
Location/Qualifiers
source 1..170
/organism="uncultured gamma proteobacterium"
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/country="Canada; Novia Scotia"
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rRNA bioremediation field study conducted at a coastal marsh"
<1..>170
BASE COUNT 47 a 36 c 52 g 35 t
ORIGIN

Query Match 91.6%; Score 17.4; DB 1; Length 170;
Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TAATGTCATCGTCCCGGG 19
Db |||||||||||
147 TAATGTCATCGTCCCGGG 129

Search completed: August 20, 2003, 03:40:56
Job time : 71.3884 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 19, 2003, 22:24:34 ; Search time 5.79223 Seconds  
(without alignments)  
8854.845 Million cell updates/sec

Title: US-09-979-558a-2

Perfect score: 19  
Sequence: 1 taatgtcatcgtccocggg 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	19	100.0	19	22 AAC87532	Psychrobacter paci
2	19	100.0	1526	22 AAC87531	Psychrobacter paci
3	16.4	86.3	584	21 AAC76269	Human OREF ORF1824
4	16.4	86.3	1882	21 AAF21914	Human breast and o
5	16.4	86.3	1926	22 ABA06572	Human cDNA SPO ID
6	16.4	86.3	1926	24 ABV83909	Human polynucleoti
7	16.4	86.3	1987	21 AA523368	NSEQ gene-20 assoc
8	16.4	86.3	1987	24 AAL42464	Human matrix-remod

9	16.4	86.3	1989	21 AAA37044	Human PRO1293 (UNC
10	16.4	86.3	1989	22 AAF54255	DNA encoding prote
11	16.4	86.3	1990	21 AAC58113	Human PRO1293 nucl
12	16.4	86.3	2005	22 AAH13666	Human cDNA sequenc
13	16.4	86.3	2132	21 AAC67985	Human MTC48 nucleo
14	16.4	86.3	2132	21 AAC76236	Human OREF ORF1791
15	16.4	86.3	2252	22 AAD12573	Human protein havi
16	16.4	86.3	2443	25 ABS57548	Human SECP-4 cDNA
17	16.4	86.3	2619	25 ABS57567	Human SECP-23 cDNA
c 18	16.4	86.3	3152	22 AAS28912	Human immunoglobul
c 19	15.8	83.2	268	25 ABX49528	Bovine EST associa
c 20	15.8	83.2	286	25 ABX36977	Bovine EST associa
c 21	15.8	83.2	286	25 ABX38622	Bovine EST associa
c 22	15.8	83.2	286	25 ABX43845	Bovine EST associa
c 23	15.8	83.2	286	25 ABX45011	Bovine EST associa
c 24	15.8	83.2	286	25 ABX45961	Bovine EST associa
c 25	15.8	83.2	286	25 ABX48337	Bovine EST associa
c 26	15.8	83.2	286	25 ABX48361	Bovine EST associa
c 27	15.8	83.2	287	25 ABX36471	Bovine EST associa
c 28	15.8	83.2	288	25 ABX45976	Bovine EST associa
c 29	15.8	83.2	290	25 ABX45470	Bovine EST associa
c 30	15.8	83.2	291	25 ABX35792	Bovine EST associa
c 31	15.8	83.2	292	25 ABX37207	Bovine EST associa
c 32	15.8	83.2	298	25 ABX37182	Bovine EST associa
c 33	15.8	83.2	298	25 ABX41972	Bovine EST associa
c 34	15.8	83.2	298	25 ABX42439	Bovine EST associa
c 35	15.8	83.2	302	25 ABX45259	Bovine EST associa
c 36	15.8	83.2	302	25 ABX46192	Bovine EST associa
c 37	15.8	83.2	303	25 ABX36021	Bovine EST associa
c 38	15.8	83.2	303	25 ABX37441	Bovine EST associa
c 39	15.8	83.2	310	25 ABX37185	Bovine EST associa
c 40	15.8	83.2	398	25 ABX35085	Bovine EST associa
c 41	15.8	83.2	404	25 ABX37912	Bovine EST associa
c 42	15.8	83.2	800	22 AAH05517	Human cDNA clone (
c 43	15.8	83.2	5504	20 AAX20559	Polynucleotide seq
c 44	15.4	81.1	488	20 AAX29126	Polynucleotide RTP
c 45	15.4	81.1	576	22 AAH67217	C glutamicum codin

ALIGNMENTS

RESULT 1  
AAC87532  
ID AAC87532 standard; DNA; 19 BP.  
XX  
AC AAC87532;  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Psychrobacter pacificensis 16S rDNA probe, SEQ ID NO:2.  
XX  
KW 16S rDNA; species-specific detection; identification;  
KW psychrophilic bacterium; oceanic circulation; Psychrobacter;  
KW probe; ss.  
XX  
XX Psychrobacter pacificensis.  
XX  
PN WO200071705-A1.  
XX  
PD 30-NOV-2000.  
XX  
PF 25-MAY-2000; 2000WO-JP03372.  
XX  
PR 25-MAY-1999; 99JP-0145342.  
PR 30-MAR-2000; 2000WO-JP02045.  
PR (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.  
PI Maruyama A, Kitamura K, Kurane R;  
XX  
DR WPI; 2001-025158/03.  
XX



PT DNA probe originating from psychrotrophic bacterium applicable in  
PT species-specific detection of the microorganism as indication in  
PT studying and monitoring its growth and circulation of deep-sea water  
PT with sensitivity -

XX Claim 3; Page 10; 37pp; Japanese.

XX The invention relates to a 1526 bp Psychrobacter pacificensis 16S rDNA  
CC sequence (AAC87531) and an oligonucleotide probe (AAC87532) comprising  
CC part of the Psychrobacter pacificensis 16S rDNA sequence which are used  
CC for monitoring the growth of psychrophilic bacteria and the circulation  
CC of deep-sea water. Psychrobacter pacificensis is an aerobic,  
CC Gram-negative, non-motile, non-spore-forming oxidase-positive bacterium  
CC originally isolated from the Japan Trench. The invention also relates to  
CC a novel method for detecting or specifically identifying Psychrobacter  
CC pacificensis, Psychrobacter glacincola, and related species, or  
CC Psychrobacter pacificensis only via the use of the 16S rDNA sequence.  
CC The 16S rDNA sequence and derived oligonucleotide probe are useful for  
CC the species-specific detection of Psychrobacter pacificensis to study  
CC and monitor its growth as an indicator of the circulation of deep-sea  
CC water. The method of the invention is rapid, accurate and has high  
CC sensitivity, and removes the need to separate and culture the biological  
CC materials. The present sequence represents a specifically claimed  
CC Psychrobacter pacificensis 16S rDNA oligonucleotide probe.

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SQ Sequence 19 BP; 3 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 19; DB 22; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TAATGTCATGTCCTCCCGG 19

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ID AAC87531 standard; DNA; 1526 BP.

XX  
AC AAC87531;  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Psychrobacter pacificensis NIBH P2K6 16S rDNA, SEQ ID NO:1.  
XX  
KW 16S rDNA; species-specific detection; identification;  
KW psychrophilic bacterium; oceanic circulation; Psychrobacter;  
KW strain NIBH P2K6; ds.  
XX  
OS Psychrobacter pacificensis.  
XX  
PN WO200071705-A1.  
XX  
PD 30-NOV-2000.  
XX  
PF 25-MAY-2000; 2000WO-JP03372.  
XX  
PR 25-MAY-1999; 99JP-0145342.  
XX  
PR 30-MAR-2000; 2000WO-JP02045.  
XX  
XX (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.  
XX  
XX Maruyama A, Kitamura K, Kurane R;  
XX  
XX WPI; 2001-025158/03.  
XX  
XX DNA probe originating from psychrotrophic bacterium applicable in  
XX species-specific detection of the microorganism as indication in  
XX studying and monitoring its growth and circulation of deep-sea water  
XX with sensitivity -

XX Claim 1; Page 30; 37pp; Japanese.

XX The invention relates to a 1526 bp Psychrobacter pacificensis 16S rDNA  
CC sequence (AAC87531) and an oligonucleotide probe (AAC87532) comprising  
CC part of the Psychrobacter pacificensis 16S rDNA sequence which are used  
CC for monitoring the growth of psychrophilic bacteria and the circulation  
CC of deep-sea water. Psychrobacter pacificensis is an aerobic,  
CC Gram-negative, non-motile, non-spore-forming oxidase-positive bacterium  
CC originally isolated from the Japan Trench. The invention also relates to  
CC a novel method for detecting or specifically identifying Psychrobacter  
CC pacificensis, Psychrobacter glacincola, and related species, or  
CC Psychrobacter pacificensis only via the use of the 16S rDNA sequence.  
CC The 16S rDNA sequence and derived oligonucleotide probe are useful for  
CC the species-specific detection of Psychrobacter pacificensis to study  
CC and monitor its growth as an indicator of the circulation of deep-sea  
CC water. The method of the invention is rapid, accurate and has high  
CC sensitivity, and removes the need to separate and culture the biological  
CC materials. The present sequence represents the Psychrobacter  
CC pacificensis 16S rDNA.

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SQ Sequence 1526 BP; 401 A; 332 C; 467 G; 323 T; 3 other;

Query Match 100.0%; Score 19; DB 22; Length 1526;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 476 TAATGTCATGTCCTCCCGG 458

RESULT 3  
AAC76269  
ID AAC76269 standard; cDNA; 584 BP.

XX  
AC AAC76269;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human ORF1824 polynucleotide sequence SEQ ID NO:3647.  
XX  
XX Human; open reading frame; ORF; detection; cytostatic; hepatotropic;  
KW vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;  
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;  
KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;  
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
KW cholesterol ester storage; systemic lupus erythematosus; infection;  
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
KW thrombosis; contraceptive; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200058473-A2.  
XX  
PD 05-OCT-2000.  
XX  
XX 31-MAR-2000; 2000WO-US08621.  
XX  
XX 31-MAR-1999; 99US-0127607.  
XX  
XX 02-APR-1999; 99US-0127636.  
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XX 05-APR-1999; 99US-0127728.  
XX  
XX 30-MAR-2000; 2000US-0540763.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shinketsu RA, Leach M;  
XX  
XX WPI; 2000-602362/57.

DR P-PSDB; AAB42060.

XX Novel nucleic acids and peptides derived from open reading frame X,

PT useful for treating e.g. cancers, proliferative disorders,

PT neurodegenerative disorders and cardiovascular disease -

XX

PS Claim 5; Page 2803; 5507pp; English.

XX

CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,

CC which represent the human ORFX open reading frames 1 to 3161. The ORFX

CC sequences have activities such as: cytostatic; hepatotropic; vulnaric;

CC antiproliferative; antiparasitic; antitumor; neuroprotective;

CC osteoprotective; anticonvulsant; antiarthritic; immunosuppressive;

CC immunostimulant; cardiac; thrombolytic; coagulant; vasotropic;

CC antidiabetic; hypotensive; dermatological; immunosuppressive;

CC antineoplastic; antibacterial; antiviral; antifungal; antirheumatic;

CC antithyroid; and antianemic. The sequences can be used for determining

CC the presence of or predisposition to, or preventing or treating

CC pathological conditions associated with an ORFX-associated disorder. The

CC nucleic acids can be used to express ORFX proteins in gene therapy

CC vectors. The proteins and nucleic acids may be used to treat cancers,

CC proliferative disorders, neurodegenerative disorders, osteoarthritis,

CC graft vs host disease, cardiovascular disease, diabetes mellitus,

CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus

CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,

CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,

CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,

CC nocturnal haemoglobinuria, anti-inflammatory disease; to enhance

CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX

SQ Sequence 584 BP; 74 A; 232 C; 183 G; 93 T; 2 other;

Query Match 86.3%; Score 16.4; DB 21; Length 584;

Best Local Similarity 94.4%; Pred. No. 98;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 AATGTCATCGTCCCGG 19

DB 480 AATGTCATCGTCCCGGAG 497

RESULT 4

AAB21914

ID AAB21914 standard; DNA; 1882 BP.

XX AC AAB21914;

XX

DT 27-MAR-2001 (first entry)

XX

DE Human breast and ovarian cancer associated antigen gene SEQ ID 301.

XX

KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;

KW neurotropic; neuroprotective; antiviral; antiallergic; hepatotropic;

KW antidiabetic; antineoplastic; antitumor; antitumor; anticonvulsant;

KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;

KW Addison's disease; allergy; autoimmune haemolytic anaemia;

KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;

KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;

KW cardiovascular disorder; wound healing; neurological disease; ds.

XX

OS Homo sapiens.

XX

PN WO200055173-A1.

XX

PD 21-SEP-2000.

XX

PF 08-MAR-2000; 2000NO-US05881.

XX

PR 12-MAR-1999; 99US-0124270.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Ruben SM;

XX WPI; 2000-611515/58.

DR P-PSDB; AAB59011.

XX

PT New human breast and ovarian cancer associated gene sequences and the

PT polypeptides encoded by these genes, useful in the prevention,

PT treatment and diagnosis of cancer, immune disorders, cardiovascular

PT disorders and neurological diseases -

XX

PS Claim 1; Page 712-713; 1299pp; English.

XX

CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human

CC proteins AAB58711 - AAB59128. The DNA and protein sequences are

CC associated with breast and ovarian cancer. Included in the invention are

CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the

CC isolation and characterisation of the DNA and protein sequences of the

CC invention. The breast and ovarian cancer associated DNA, protein, agonist

CC or antagonist sequences exhibit cytostatic; immunosuppressive;

CC neurotropic; neuroprotective; antiviral; antiallergic; hepatotropic;

CC antidiabetic; antineoplastic; antitumor; antitumor; anticonvulsant;

CC antibacterial; antifungal; antiparasitic and cardiac activity. The

CC polynucleotide and protein sequences are used in the diagnosis of cancer,

CC particularly breast and ovarian cancer. The nucleic acid sequences,

CC proteins, agonists and antagonists may also be used in the diagnosis,

CC prevention and treatment of immune disorders e.g. Addison's disease,

CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,

CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid

CC arthritis and ulcerative colitis; cardiovascular disorders such as

CC myocardial ischaemia; wound healing; neurological diseases such as

CC cerebral anoxia and epilepsy; and infectious diseases.

XX

SQ Sequence 1882 BP; 383 A; 616 C; 527 G; 350 T; 6 other;

Query Match 86.3%; Score 16.4; DB 21; Length 1882;

Best Local Similarity 94.4%; Pred. No. 1.1e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 AATGTCATCGTCCCGG 19

DB 529 AATGTCATCGTCCCGGAG 546

RESULT 5

AAB06572

ID AAB06572 standard; cDNA; 1926 BP.

XX AC AAB06572;

XX

DT 10-JAN-2002 (first entry)

XX

DE Human cDNA SEQ ID NO: 238.

XX

KW Human; gene therapy; neural disorder; immune system disorder;

KW muscular disorder; reproductive disorder; gastrointestinal disorder;

KW pulmonary disorder; cardiovascular disorder; renal disorder;

KW proliferative disorder; inflammation; ss.

XX

OS Homo sapiens.

XX

PN WO200154474-A2.

XX

PD 02-AUG-2001.

XX

PF 17-JAN-2001; 2001WO-US01349.

XX

PR 31-JAN-2000; 2000US-179065P.

PR 04-FEB-2000; 2000US-180628P.

PR 24-FEB-2000; 2000US-184664P.

PR 02-MAR-2000; 2000US-186350P.

PR 16-MAR-2000; 2000US-189874P.

PR 17-MAR-2000; 2000US-190076P.

PR 18-APR-2000; 2000US-198123P.

PR 19-MAY-2000; 2000US-205515P.

PR 07-JUN-2000; 2000US-209457P.  
PR 28-JUN-2000; 2000US-214886P.  
PR 30-JUN-2000; 2000US-215135P.  
PR 07-JUL-2000; 2000US-216547P.  
PR 07-JUL-2000; 2000US-216880P.  
PR 11-JUL-2000; 2000US-217487P.  
PR 11-JUL-2000; 2000US-217496P.  
PR 14-JUL-2000; 2000US-218290P.  
PR 26-JUL-2000; 2000US-220963P.  
PR 26-JUL-2000; 2000US-220964P.  
PR 14-AUG-2000; 2000US-224518P.  
PR 14-AUG-2000; 2000US-224519P.  
PR 14-AUG-2000; 2000US-225213P.  
PR 14-AUG-2000; 2000US-225214P.  
PR 14-AUG-2000; 2000US-225266P.  
PR 14-AUG-2000; 2000US-225267P.  
PR 14-AUG-2000; 2000US-225268P.  
PR 14-AUG-2000; 2000US-225270P.  
PR 14-AUG-2000; 2000US-225447P.  
PR 14-AUG-2000; 2000US-225757P.  
PR 14-AUG-2000; 2000US-225758P.  
PR 14-AUG-2000; 2000US-225759P.  
PR 18-AUG-2000; 2000US-226279P.  
PR 22-AUG-2000; 2000US-226681P.  
PR 22-AUG-2000; 2000US-226686P.  
PR 22-AUG-2000; 2000US-227182P.  
PR 23-AUG-2000; 2000US-227009P.  
PR 30-AUG-2000; 2000US-228924P.  
PR 01-SEP-2000; 2000US-229287P.  
PR 01-SEP-2000; 2000US-229343P.  
PR 01-SEP-2000; 2000US-229344P.  
PR 01-SEP-2000; 2000US-229345P.  
PR 05-SEP-2000; 2000US-229509P.  
PR 05-SEP-2000; 2000US-229513P.  
PR 06-SEP-2000; 2000US-230437P.  
PR 06-SEP-2000; 2000US-230438P.  
PR 08-SEP-2000; 2000US-231242P.  
PR 08-SEP-2000; 2000US-231243P.  
PR 08-SEP-2000; 2000US-231244P.  
PR 08-SEP-2000; 2000US-231413P.  
PR 08-SEP-2000; 2000US-231414P.  
PR 08-SEP-2000; 2000US-232080P.  
PR 08-SEP-2000; 2000US-232081P.  
PR 12-SEP-2000; 2000US-231968P.  
PR 14-SEP-2000; 2000US-232397P.  
PR 14-SEP-2000; 2000US-232398P.  
PR 14-SEP-2000; 2000US-232399P.  
PR 14-SEP-2000; 2000US-232400P.  
PR 14-SEP-2000; 2000US-232401P.  
PR 14-SEP-2000; 2000US-233063P.  
PR 14-SEP-2000; 2000US-233064P.  
PR 14-SEP-2000; 2000US-233065P.  
PR 21-SEP-2000; 2000US-234223P.  
PR 21-SEP-2000; 2000US-234274P.  
PR 25-SEP-2000; 2000US-234997P.  
PR 25-SEP-2000; 2000US-234998P.  
PR 26-SEP-2000; 2000US-235484P.  
PR 27-SEP-2000; 2000US-235834P.  
PR 27-SEP-2000; 2000US-235836P.  
PR 29-SEP-2000; 2000US-236327P.  
PR 29-SEP-2000; 2000US-236367P.  
PR 29-SEP-2000; 2000US-236368P.  
PR 29-SEP-2000; 2000US-236369P.  
PR 29-SEP-2000; 2000US-236370P.  
PR 02-OCT-2000; 2000US-236802P.  
PR 02-OCT-2000; 2000US-237037P.  
PR 02-OCT-2000; 2000US-237038P.  
PR 02-OCT-2000; 2000US-237039P.  
PR 02-OCT-2000; 2000US-237040P.  
PR 13-OCT-2000; 2000US-239955P.  
PR 13-OCT-2000; 2000US-239957P.  
PR 20-OCT-2000; 2000US-240960P.  
PR 20-OCT-2000; 2000US-241221P.

PR 20-OCT-2000; 2000US-241785P.  
PR 20-OCT-2000; 2000US-241786P.  
PR 20-OCT-2000; 2000US-241787P.  
PR 20-OCT-2000; 2000US-241808P.  
PR 20-OCT-2000; 2000US-241809P.  
PR 20-OCT-2000; 2000US-241826P.  
PR 01-NOV-2000; 2000US-244617P.  
PR 08-NOV-2000; 2000US-246474P.  
PR 08-NOV-2000; 2000US-246475P.  
PR 08-NOV-2000; 2000US-246476P.  
PR 08-NOV-2000; 2000US-246477P.  
PR 08-NOV-2000; 2000US-246478P.  
PR 08-NOV-2000; 2000US-246523P.  
PR 08-NOV-2000; 2000US-246524P.  
PR 08-NOV-2000; 2000US-246525P.  
PR 08-NOV-2000; 2000US-246526P.  
PR 08-NOV-2000; 2000US-246527P.  
PR 08-NOV-2000; 2000US-246528P.  
PR 08-NOV-2000; 2000US-246532P.  
PR 08-NOV-2000; 2000US-246609P.  
PR 08-NOV-2000; 2000US-246610P.  
PR 08-NOV-2000; 2000US-246611P.  
PR 08-NOV-2000; 2000US-246613P.  
PR 17-NOV-2000; 2000US-249207P.  
PR 17-NOV-2000; 2000US-249208P.  
PR 17-NOV-2000; 2000US-249209P.  
PR 17-NOV-2000; 2000US-249210P.  
PR 17-NOV-2000; 2000US-249211P.  
PR 17-NOV-2000; 2000US-249212P.  
PR 17-NOV-2000; 2000US-249213P.  
PR 17-NOV-2000; 2000US-249214P.  
PR 17-NOV-2000; 2000US-249215P.  
PR 17-NOV-2000; 2000US-249216P.  
PR 17-NOV-2000; 2000US-249217P.  
PR 17-NOV-2000; 2000US-249218P.  
PR 17-NOV-2000; 2000US-249244P.  
PR 17-NOV-2000; 2000US-249245P.  
PR 17-NOV-2000; 2000US-249264P.  
PR 17-NOV-2000; 2000US-249265P.  
PR 17-NOV-2000; 2000US-249297P.  
PR 17-NOV-2000; 2000US-249299P.  
PR 17-NOV-2000; 2000US-249300P.  
PR 01-DEC-2000; 2000US-250160P.  
PR 01-DEC-2000; 2000US-250391P.  
PR 05-DEC-2000; 2000US-251030P.  
PR 05-DEC-2000; 2000US-251988P.  
PR 05-DEC-2000; 2000US-256719P.  
PR 06-DEC-2000; 2000US-251479P.  
PR 08-DEC-2000; 2000US-251856P.  
PR 08-DEC-2000; 2000US-251868P.  
PR 08-DEC-2000; 2000US-251869P.  
PR 08-DEC-2000; 2000US-251989P.  
PR 08-DEC-2000; 2000US-251990P.  
PR 11-DEC-2000; 2000US-254097P.  
PR 05-JAN-2001; 2001US-259678P.  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
PI  
XX  
XX WPI; 2001-476161/51.  
XX P-PSDB; ABB10350.  
XX  
XX Isolated nucleic acid molecule encoding an inflammation-associated  
PT polypeptide is used in preventing, treating or ameliorating a medical  
PT condition -  
XX  
XX Claim 1; SEQ ID NO: 238; 859pp + Sequence Listing; English.  
XX  
XX The present invention provides human cDNAs, proteins and related genomic  
CC DNAs. These can be used in the treatment of neural, immune system,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal and proliferative disorders and inflammation. The present sequence

CC is a cDNA of the invention.

XX Sequence 1926 BP; 395 A; 654 C; 536 G; 341 T; 0 other;

SO Query Match 86.3%; Score 16.4; DB 22; Length 1926;

Best Local Similarity 94.4%; Pred. No. 1.1e-02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 AATGTCATCGTCCCGGG 19

|||||

573 AATGTCATCGTCCCGAG 590

# RESULT 6

ABV83909

ID ABV83909 standard; cDNA; 1926 BP.

AC ABV83909;

XX 09-DEC-2002 (first entry)

DE Human polynucleotide SEQ ID NO 238.

XX Human; nontropic; neuroprotective; cytostatic; dermatological; virucide;  
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;  
 KW antiparkinsonian; antickling; antianemic; antiarthritic; cancer;  
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;  
 KW antidiabetic; antihyperlipidemic; anticonvulsant; antifungal;  
 KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine;  
 XX gene; ss.

XX Homo sapiens.

OS US2002090672-A1.

PN 11-JUL-2002.

PD 17-JAN-2001; 2001US-0764853.

PF 31-JAN-2000; 2000US-179065P.

PR 04-FEB-2000; 2000US-180628P.

PR 28-JUN-2000; 2000US-214886P.

PR 07-JUL-2000; 2000US-215647P.

PR 07-JUL-2000; 2000US-215680P.

PR 11-JUL-2000; 2000US-217487P.

PR 11-JUL-2000; 2000US-217496P.

PR 14-JUL-2000; 2000US-218290P.

PR 26-JUL-2000; 2000US-220963P.

PR 26-JUL-2000; 2000US-220964P.

PR 14-AUG-2000; 2000US-224518P.

PR 14-AUG-2000; 2000US-224519P.

PR 14-AUG-2000; 2000US-225267P.

PR 14-AUG-2000; 2000US-225268P.

PR 14-AUG-2000; 2000US-225270P.

PR 14-AUG-2000; 2000US-225447P.

PR 14-AUG-2000; 2000US-225757P.

PR 14-AUG-2000; 2000US-225758P.

PR 30-AUG-2000; 2000US-228924P.

PR 01-SEP-2000; 2000US-229287P.

PR 01-SEP-2000; 2000US-229343P.

PR 01-SEP-2000; 2000US-229344P.

PR 01-SEP-2000; 2000US-229345P.

PR 05-SEP-2000; 2000US-229509P.

PR 05-SEP-2000; 2000US-229513P.

PR 08-SEP-2000; 2000US-231413P.

PR 21-SEP-2000; 2000US-234223P.

PR 21-SEP-2000; 2000US-234274P.

PR 25-SEP-2000; 2000US-234997P.

PR 27-SEP-2000; 2000US-235834P.

PR 29-SEP-2000; 2000US-236327P.

PR 29-SEP-2000; 2000US-236367P.

PR 29-SEP-2000; 2000US-236368P.  
 PR 29-SEP-2000; 2000US-236369P.  
 PR 29-SEP-2000; 2000US-236370P.  
 PR 02-OCT-2000; 2000US-236802P.  
 PR 02-OCT-2000; 2000US-237037P.  
 PR 02-OCT-2000; 2000US-237038P.  
 PR 02-OCT-2000; 2000US-237039P.  
 PR 02-OCT-2000; 2000US-237040P.  
 PR 13-OCT-2000; 2000US-239935P.  
 PR 20-OCT-2000; 2000US-240960P.  
 PR 20-OCT-2000; 2000US-241785P.  
 PR 20-OCT-2000; 2000US-241809P.  
 PR 01-NOV-2000; 2000US-244617P.  
 PR 17-NOV-2000; 2000US-249299P.  
 PR 08-DEC-2000; 2000US-251856P.  
 PR 08-DEC-2000; 2000US-251868P.  
 PR 08-DEC-2000; 2000US-251869P.

PA (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.

PA (BARA/) BARASH S C.

XX Rosen CA, Ruben SM, Barash SC;

PI WPI: 2002-681727/73.

XX P-PSDB; ABP66937.

DR Novel polypeptide useful for diagnosis, prognosis, prevention, and

XX treatment of immune, hyperproliferative, renal, respiratory,

PT cardiovascular, reproductive, endocrine, gastrointestinal and

PT neurological disorders

XX Claim 1; SEQ ID NO 238; 369pp + Sequence Listing; English.

PS The invention relates to novel genes (ABV83682-ABV84101) and proteins

XX (ABP66710-ABP67129) useful for preventing, treating or ameliorating

CC medical conditions e.g. by protein or gene therapy. The genes are

CC isolated from a range of human tissues disclosed in the specification.

CC The nucleic acids, proteins, antibodies and (ant)agonists are useful

CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast

CC and ovarian cancer and other cancers of the adrenal gland, bone, bone

CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;

CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune

CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's

CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative

CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;

CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and

CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal

CC and parasitic infections.

CC Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 1926 BP; 395 A; 654 C; 536 G; 341 T; 0 other;

Query Match 86.3%; Score 16.4; DB 24; Length 1926;

Best Local Similarity 94.4%; Pred. No. 1.1e-02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 AATGTCATCGTCCCGGG 19

|||||

573 AATGTCATCGTCCCGAG 590

# RESULT 7

AAZ52368

ID AAZ52368 standard; cDNA; 1987 BP.

XX AAZ52368;

XX 24-JUL-2000 (first entry)

DT NSEQ gene-20 associated with matrix remodelling.

XX

DE

XX NSEQ gene; matrix-remodeling gene; Incyte clone 3948614; cancer;  
 KW matrix-remodeling disease; cardiomyopathy; arthritis; angiogenesis;  
 KW diabetic necrosis; atherosclerosis; fibrosis; ulceration; cytostatic;  
 KW cardioactive; antiarthritic; angiogenic; antiarteriosclerotic;  
 KW antiulcer; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200021986-A2.  
 PN  
 XX 20-APR-2000.  
 PD  
 XX 06-OCT-1999; 99WO-US23315.  
 XX  
 PF  
 XX 09-OCT-1998; 98US-0169289.  
 XX  
 PR  
 XX (INCY-) INCYTE PHARM INC.  
 PA  
 XX Walker MG, Volkmath W, Klingler TM;  
 PI WPI; 2000-317934/27.  
 XX  
 DR Protein co-expressed with matrix-remodeling proteins, useful in the  
 XX diagnosis and treatment of cancer, cardiomyopathy, arthritis,  
 PT angiogenesis, diabetic necrosis, atherosclerosis, fibrosis, and  
 PT ulceration.  
 PT  
 XX Claim 1; Page 51-52; 55pp; English.  
 PS  
 XX The present sequence is NSEQ gene that is co-expressed with one or more  
 CC known matrix-remodeling genes in a number of biological samples using an  
 CC expression vector. This sequence was identified from the  
 CC Incyte clone 3948614. The gene, protein, and antibody sequences can be  
 CC used in the diagnosis, and treatment or prevention of a disease  
 CC associated with its altered expression. The diseases that can be treated  
 CC are matrix-remodeling diseases, including cancer, cardiomyopathy,  
 CC arthritis, angiogenesis, diabetic necrosis, atherosclerosis, fibrosis,  
 CC and ulceration.  
 CC  
 XX Sequence 1987 BP; 345 A; 597 C; 579 G; 366 T; 0 other;  
 SQ  
 Query Match 86.3%; Score 16.4; DB 21; Length 1987;  
 Best Local Similarity 94.4%; Pred. No. 1.1e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 AATGTCATCGTCCCGG 19  
 DB 716 AATGTCATCGTCCCGGAG 733  
 RESULT 8  
 ID AAL42464 standard; DNA; 1987 BP.  
 AC AAL42464;  
 XX  
 XX 11-JUL-2002 (first entry)  
 DT  
 XX Human matrix-remodeling-associated nucleotide 20.  
 DE  
 XX Human; ds; matrix-remodeling gene; extracellular matrix; gene;  
 KW matrix-remodeling-associated nucleotide; screening;  
 KW matrix remodeling-associated disease; angiogenesis; arthritis;  
 KW atherosclerosis; cancer; cardiomyopathy; diabetic necrosis; fibrosis;  
 KW ulceration.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2002019000-A1.  
 PN  
 XX 14-FEB-2002.  
 PD  
 XX

PF 26-MAR-2001; 2001US-0818143.  
 XX  
 XX 09-OCT-1998; 98US-0169289.  
 PR  
 XX (WALK/) WALKER M G.  
 PA (VOLK/) VOLKMAT W.  
 PA (KLIN/) KLINGLER T M.  
 XX  
 XX Walker MG, Volkmath W, Klingler TM;  
 PI WPI; 2002-338319/37.  
 DR  
 XX New isolated polynucleotide coexpressed with matrix-remodeling genes,  
 PT useful in diagnosis, prognosis, prevention and treatment of diseases  
 PT associated with matrix-remodeling such as angiogenesis, arthritis and  
 PT cancer.  
 PT  
 XX Claim 2; Page 36-37; 63pp; English.  
 PS  
 XX The invention comprises human nucleotide sequences which are co-expressed  
 CC with matrix-remodeling genes. Matrix-remodeling is associated with the  
 CC construction, destruction and reorganisation of extracellular matrix  
 CC components. The matrix-remodeling-associated nucleotides of the invention  
 CC are useful for screening for and purifying ligands that specifically bind  
 CC to the nucleotides of the invention. The matrix-remodeling-associated  
 CC nucleotides of the invention are also useful in the diagnosis, prognosis,  
 CC prevention, treatment and evaluation of therapies for diseases associated  
 CC with matrix remodelling (e.g. angiogenesis, arthritis, atherosclerosis,  
 CC cancer, cardiomyopathy, diabetic necrosis, fibrosis and ulceration). The  
 CC present DNA sequence represents a human matrix-remodeling-associated  
 CC nucleotide of the invention.  
 CC  
 XX Sequence 1987 BP; 345 A; 597 C; 579 G; 366 T; 0 other;  
 SQ  
 Query Match 86.3%; Score 16.4; DB 24; Length 1987;  
 Best Local Similarity 94.4%; Pred. No. 1.1e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 AATGTCATCGTCCCGG 19  
 DB 716 AATGTCATCGTCCCGGAG 733  
 RESULT 9  
 ID AAA37044 standard; cDNA; 1989 BP.  
 XX  
 XX AAA37044;  
 AC  
 XX 08-AUG-2000 (first entry)  
 DT  
 XX Human PRC1293 (UNQ662) cDNA sequence SEQ ID NO:76.  
 DE  
 XX Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
 KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening;  
 KW ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO2000012708-A2.  
 PN  
 XX 09-MAR-2000.  
 PD  
 XX 01-SEP-1999; 99WO-US20111.  
 PF  
 XX 01-SEP-1998; 98US-0098716.  
 PR 01-SEP-1998; 98US-0098749.  
 PR 01-SEP-1998; 98US-0098750.  
 PR 02-SEP-1998; 98US-0098803.  
 PR 02-SEP-1998; 98US-0098821.  
 PR 02-SEP-1998; 98US-0098843.  
 PR 09-SEP-1998; 98US-0099536.  
 PR 09-SEP-1998; 98US-0099596.



Db 715 AATGTCATCGTCCCGAG 732

RESULT 10  
AAF54255  
ID AAF54255 standard; DNA; 1989 BP.  
XX  
XX AAF54255;  
AC  
XX 02-APR-2001 (first entry)  
XX  
XX DNA encoding protein of the invention #23.  
XX  
XX  
XX Secreted; transmembrane; gene therapy; ss.  
XX  
XX Unidentified.  
XX  
XX W0200078961-A1.  
XX  
XX 28-DEC-2000.  
PD  
XX  
XX 18-FEB-2000; 2000WO-US04342.  
PF  
XX  
XX 23-JUN-1999; 99US-0141037.  
PR  
XX 20-JUL-1999; 99US-0144758.  
PR  
XX 26-JUL-1999; 99US-0145698.  
PR  
XX 01-SEP-1999; 99WO-US20111.  
PR  
XX 29-OCT-1999; 99US-0162506.  
PR  
XX 30-NOV-1999; 99WO-US28313.  
PR  
XX 02-DEC-1999; 99WO-US28551.  
PR  
XX 16-DEC-1999; 99WO-US30095.  
PR  
XX 05-JAN-2000; 2000WO-US00219.  
PR  
XX 06-JAN-2000; 2000WO-US00376.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI  
XX Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
PI  
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;  
PI  
XX Watanabe CK, Williams PM, Wood WI;  
XX  
XX WPI; 2001-071395/08.  
DR  
XX  
XX Secreted and transmembrane proteins and nucleic acids designated PRO,  
PT  
XX useful as hybridization probes, in chromosome and gene mapping and gene  
PT  
XX therapy -  
XX  
XX Claim 2; Fig 45; 787pp; English.  
FS  
XX  
XX The present invention relates to secreted and transmembrane proteins.  
CC  
XX These proteins and the DNA encoding them may be used as hybridization  
CC  
XX probes, in chromosome and gene mapping and in the generation of  
CC  
XX anti-sense RNA and DNA. They may also be used to generate either  
CC  
XX transgenic animals or knockout animals which are in turn useful for  
CC  
XX development and screening of therapeutically useful reagents.  
CC  
XX The nucleic acids may also be used in gene therapy.  
XX  
XX Sequence 1989 BP; 340 A; 693 C; 586 G; 370 T; 0 other;  
SQ  
XX  
XX Query Match 86.3%; Score 16.4; DB 22; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 1.1e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 AATGTCATCGTCCCGGG 19  
|||||  
Db 715 AATGTCATCGTCCCGAG 732  
RESULT 11  
AAC58113  
ID AAC58113 standard; cDNA; 1990 BP.  
XX  
XX AAC58113;  
AC

XX 25-JAN-2001 (first entry)  
XX  
XX Human PRO1293 nucleotide sequence SEQ ID NO:30.  
XX  
XX Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;  
KW identification; tumorigenesis; anticancer; detection; ss.  
XX  
XX Homo sapiens.  
OS  
XX W0200053750-A1.  
XX  
XX 14-SEP-2000.  
PD  
XX  
XX 02-DEC-1999; 99WO-US28551.  
PF  
XX  
XX 08-MAR-1999; 99WO-US05028.  
PR  
XX 01-SEP-1999; 99WO-US20111.  
PR  
XX 23-OCT-1999; 99US-0162506.  
PR  
XX 30-NOV-1999; 99WO-US28313.  
PR  
XX 01-DEC-1999; 99WO-US28634.  
PR  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;  
PI  
XX WPI; 2000-594320/56.  
DR  
XX P-PSDB; AAB24031.  
XX  
XX Antibodies specific for PRO polypeptides, used to diagnose and inhibit  
PT the growth of tumors in mammals, and to identify inhibitors of PRO  
PT polypeptide activity or expression -  
XX  
XX Claim 50; Fig 21; 226pp; English.  
FS  
XX  
XX The present invention describes an antibody that binds to a human  
CC protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780;  
CC PRO3434; PRO1927; PRO3567; PRO1293; PRO1303; PRO4344; PRO4354;  
CC PRO4397; PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has  
CC anticancer activity and can be used to diagnose tumours in mammals, by  
CC detecting complex formation when the antibody is contacted with test  
CC cells. Increased expression of genes encoding (I) can also be detected  
CC to diagnose tumours. Agents which inhibit the activity of (I),  
CC especially the antibodies, or an antisense oligonucleotide which  
CC hybridises to genes encoding (I), can be used to inhibit tumour growth,  
CC preferably by inducing cell death. Methods from the present invention  
CC can be used to identify compounds which inhibit the biological activity  
CC of (I). AAC58019 to AAC58102 represent PCR primers and hybridisation  
CC probes used in examples from the present invention for human PRO  
CC sequences. AAC58103 to AAC58122 and AAB24021 to AAB24040 represent human  
CC PRO polynucleotide and protein sequences given in the exemplification of  
CC the present invention.  
XX  
XX Sequence 1990 BP; 341 A; 693 C; 586 G; 370 T; 0 other;  
SQ  
XX  
XX Query Match 86.3%; Score 16.4; DB 21; Length 1990;  
Best Local Similarity 94.4%; Pred. No. 1.1e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 AATGTCATCGTCCCGGG 19  
|||||  
Db 715 AATGTCATCGTCCCGAG 732  
RESULT 12  
AAH13666  
ID AAH13666 standard; cDNA; 2005 BP.  
XX  
XX AAH13666;  
AC  
XX  
XX 26-JUN-2001 (first entry)  
DT  
XX  
XX Human cDNA sequence SEQ ID NO:10519.  
DE



XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
 KW Homo sapiens.  
 OS EF1074617-A2.  
 PN 07-FEB-2001.  
 PD 28-JUL-2000; 2000EP-0116126.  
 PF 29-JUL-1999; 99JP-0248036.  
 PR 27-AUG-1999; 98JP-0300253.  
 PR 11-JAN-2000; 2000JP-0118776.  
 PR 02-MAY-2000; 2000JP-0183767.  
 PR 09-JUN-2000; 2000JP-0241899.  
 XX (HELI-) HELIX RES INST.  
 PA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 DR WPI; 2001-318749/34.  
 XX Primer sets for synthesizing polynucleotides, particularly the 5602  
 PT full-length cDNAs defined in the specification, and for the detection  
 PT and/or diagnosis of the abnormality of the proteins encoded by the  
 PT full-length cDNAs -  
 XX  
 PS Claim 8; SEQ ID 10519; 2537pp + CD ROM; English.  
 XX The present invention describes primer sets for synthesizing 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
 CC AAB93893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.  
 XX  
 SQ Sequence 2005 BP; 318 A; 700 C; 626 G; 361 T; 0 other;  
 Query Match 86.3%; Score 16.4; DB 22; Length 2005;  
 Best Local Similarity 94.4%; Pred. No. 1.1e-02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 2 AATGTCATGTCCTCCGGG 19  
 DB 1025 AATGTCATGTCCTCCGGG 1042  
 RESULT 13  
 AAC67985  
 ID AAC67985 standard; cDNA; 2132 BP.  
 XX AAC67985;  
 AC  
 XX  
 DT 20-FEB-2001 (first entry)  
 XX

DE Human MTC48 nucleotide sequence.  
 KW Human; cytostatic; metastatic thyroid cancer; MTC; thyroid carcinoma; ss.  
 XX Homo sapiens.  
 OS WO200063438-A2.  
 PN 26-OCT-2000.  
 PD 20-APR-2000; 2000WO-US10729.  
 PF 20-APR-1999; 99US-0130123.  
 PR 30-MAR-2000; 2000US-0193203.  
 PR 19-APR-2000; 2000US-0552322.  
 XX (CURA-) CURAGEN CORP.  
 PA Gould-Rothberg BE, Rastelli L;  
 PI WPI; 2000-565252/64.  
 DR P-PSDB; AAB36107.  
 XX  
 PT Categorizing, diagnosing or assessing the prognosis of thyroid  
 PT carcinoma by measuring the expression levels of MTC (metastatic thyroid  
 PT cancer) genes -  
 XX  
 PS Claim 1; Page 32-33; 105pp; English.  
 XX  
 CC The present sequence encodes a novel metastatic thyroid cancer (MTC)  
 CC protein. A method of categorising, diagnosing or assessing the prognosis  
 CC of thyroid carcinoma by measuring the expression levels of MTC genes is  
 CC disclosed. The MTC genes are differentially expressed in metastatic  
 CC thyroid cancer when compared to non-metastatic thyroid cancer. An  
 CC agent that decreases the expression or activity of one or more MTC genes  
 CC may be administered to treat metastatic carcinoma. Allele-specific  
 CC oligonucleotide probes that hybridise to an MTC polynucleotide at a  
 CC polymorphic site may be used to determine whether a subject suffers from  
 CC or is at risk of metastatic thyroid carcinoma.  
 XX  
 SQ Sequence 2132 BP; 360 A; 751 C; 644 G; 377 T; 0 other;  
 Query Match 86.3%; Score 16.4; DB 21; Length 2132;  
 Best Local Similarity 94.4%; Pred. No. 1.1e-02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 2 AATGTCATGTCCTCCGGG 19  
 DB 844 AATGTCATGTCCTCCGGG 861  
 RESULT 14  
 AAC676236  
 ID AAC676236 standard; cDNA; 2132 BP.  
 XX AAC676236;  
 AC  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Human ORFX ORF1791 polynucleotide sequence SEQ ID NO:3581.  
 KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
 KW vulnary; antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;  
 KW anticonvulsant; osteopathic; antiarthritis; immunosuppressant; cardiant;  
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antiinflammatory;  
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;  
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;  
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
 KW cholesterol ester storage; systemic lupus erythematosus; infection;  
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;

KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
 KW thrombosis; contraceptive; ss.  
 OS Homo sapiens.  
 XX WO2000058473-A2.  
 XX 05-OCT-2000.  
 XX 31-MAR-2000; 2000WO-US08621.  
 XX 31-MAR-1999; 99US-0127607.  
 PR 02-APR-1999; 99US-0127636.  
 PR 05-APR-1999; 99US-0127728.  
 PR 30-MAR-2000; 2000US-0540763.  
 XX (CURA-) CURAGEN CORP.  
 XX Shimkets RA, Leach M;  
 XX WPI; 2000-603362/57.  
 DR P-PSDB; AAB42027.  
 XX Novel nucleic acids and peptides derived from open reading frame X,  
 PT useful for treating e.g. cancers, proliferative disorders,  
 PT neurodegenerative disorders and cardiovascular disease -  
 XX Claim 5; Page 2741-2743; 5507pp; English.  
 XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;  
 CC antiparasitic; antiparkinsonian; nootropic; neuroprotective;  
 CC osteopathic; anticoagulant; antiarthritic; immunosuppressant;  
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;  
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;  
 CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;  
 CC antithyroid; and antianemic. The sequences can be used for determining  
 CC the presence of or predisposition to, or preventing or treating  
 CC pathological conditions associated with an ORFX-associated disorder. The  
 CC nucleic acids can be used to express ORFX proteins in gene therapy  
 CC vectors. The proteins and nucleic acids may be used to treat cancers,  
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
 CC bacterial or fungal infection; malaria, autoimmune disorders, asthma,  
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance  
 CC coagulation; to inhibit thrombosis; and as a contraceptive.  
 XX Sequence 2132 BP; 360 A; 751 C; 642 G; 377 T; 2 other;  
 SQ Query Match 86.3%; Score 16.4; DB 21; Length 2132;  
 Best Local Similarity 94.4%; Pred. No. 1.1e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 AATGTCATCGTCCCGG 19  
 |||||||  
 Db 846 AATGTCATCGTCCCGG 863  
 RESULT 15  
 AAD12573  
 ID AAD12573 standard; cDNA; 2252 BP.  
 XX AC AAD12573;  
 XX 25-SEP-2001 (first entry)  
 XX Human protein having hydrophobic domain encoding cDNA clone HP10769.  
 XX Human; hydrophobic domain; gene therapy; nutritional supplement;

KW cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;  
 KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;  
 KW haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;  
 KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;  
 KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;  
 KW contraceptive; antifertility; antiinflammatory; ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX 12..1340  
 FT CDS  
 FT /\*tag= a  
 FT /product= "Human protein having hydrophobic domain"  
 FT /note= "CDS is specifically is claimed in claim 3"  
 XX WO200149728-A2.  
 XX 12-JUL-2001.  
 XX 28-DEC-2000; 2000WO-JP09359.  
 XX 06-JAN-2000; 2000JP-0000585.  
 PR 06-JAN-2000; 2000JP-0000588.  
 PR 11-JAN-2000; 2000JP-0002299.  
 PR 03-FEB-2000; 2000JP-0026862.  
 PR 03-MAR-2000; 2000JP-0058367.  
 XX (PROT-) PROTEGENE INC.  
 XX (SAGA ) SAGAMI CHEM RES CENT.  
 XX Kato S, Kimura T;  
 XX WPI; 2001-419355/44.  
 DR P-PSDB; AAE06578.  
 XX Human proteins with hydrophobic domains and the nucleic acids encoding  
 PT them, useful for preventing diagnosing and treating e.g. cancer,  
 PT Alzheimer's and inflammation -  
 XX Claim 4; Page 282-286; 563pp; English.  
 CC The present sequence is human protein with hydrophobic domain encoding  
 CC cDNA clone HP10769. The polynucleotide and polypeptide of the invention  
 CC may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate polypeptide expression. The polynucleotides  
 CC may be used to produce the polypeptide, by inserting the nucleic acids  
 CC into a host cell and culturing the cell to express the protein. The  
 CC polynucleotides and its complementary sequences may also be used as DNA  
 CC probes in diagnostic assays and also used in gene therapy. The  
 CC polypeptides may also be used as antigens in the production of antibodies  
 CC and in assays to identify modulators of polypeptide expression and  
 CC activity. The polypeptides and nucleic acids may be used as nutritional  
 CC supplements, to modulate cytokine and cell proliferation activity, to  
 CC modulate immune stimulation or suppression (e.g. for the treatment of  
 CC microbial infections and autoimmune disorders such as multiple sclerosis,  
 CC rheumatoid arthritis and insulin-dependent diabetes), to modulate  
 CC haematopoiesis, to modulate tissue growth activity (e.g. for the  
 CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's  
 CC disease), to modulate activin and inhibin activity (e.g. for controlling  
 CC fertility), to modulate chemotactic and chemokinetic activity, to  
 CC modulate haemostatic and thrombolytic activity, to modulate receptor  
 CC ligand activity, to modulate inflammation and to inhibit tumour growth.  
 XX Sequence 2252 BP; 349 A; 798 C; 694 G; 411 T; 0 other;  
 SQ Query Match 86.3%; Score 16.4; DB 22; Length 2252;  
 Best Local Similarity 94.4%; Pred. No. 1.1e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 AATGTCATCGTCCCGG 19  
 |||||||  
 Db 993 AATGTCATCGTCCCGG 1010

Search completed: August 20, 2003, 02:03:59  
Job time : 6.75223 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 01:43:45 ; Search time 43.2142 Seconds  
(without alignments)  
10685.946 Million cell updates/sec

Title: US-09-979-558A-2  
Perfect score: 19  
Sequence: 1 taatgtcatgtcccgagg 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: em\_estba: \*  
2: em\_esthum: \*  
3: em\_estin: \*  
4: em\_estmv: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_htc: \*  
9: gb\_estl: \*  
10: gb\_est2: \*  
11: gb\_htc: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estfun: \*  
16: em\_estom: \*  
17: em\_gss\_hum: \*  
18: em\_gss\_inv: \*  
19: em\_gss\_pln: \*  
20: em\_gss\_vrt: \*  
21: em\_gss\_fun: \*  
22: em\_gss\_man: \*  
23: em\_gss\_mus: \*  
24: em\_gss\_pro: \*  
25: em\_gss\_rod: \*  
26: em\_gss\_phg: \*  
27: em\_gss\_vri: \*  
28: gb\_gss1: \*  
29: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	16.4	86.3	337	14	W92952	W92952 zd92e10.r1
C 2	16.4	86.3	340	9	AA037563	AA037563 zk34a03.i
C 3	16.4	86.3	369	14	W45082	W45082 zc21d10.r1
C 4	16.4	86.3	513	9	AA115144	AA115144 z110f09.i

C	5	16.4	86.3	533	9	AI817726	AI817726 wk25e07.x
C	6	16.4	86.3	537	14	W16559	W16559 zbl1b12.r1
C	7	16.4	86.3	539	9	AI772402	AI772402 ST9353502
C	8	16.4	86.3	554	12	BI627185	BI627185 RH8421.5
C	9	16.4	86.3	562	10	AW963853	AW963853 EST375926
C	10	16.4	86.3	595	10	BF342569	BF342569 602013893
C	11	16.4	86.3	623	9	AL680804	AL680804 AL680804
C	12	16.4	86.3	682	10	BG127540	BG127540 EST473282
C	13	16.4	86.3	768	12	BI758715	BI758715 603024016
C	14	16.4	86.3	799	12	BI754114	BI754114 603027673
C	15	16.4	86.3	903	13	BQ861886	BQ861886 AGENCOURT
C	16	16.4	86.3	957	13	BQ717752	BQ717752 AGENCOURT
C	17	16.4	86.3	1060	13	BU134659	BU134659 603121881
C	18	16.4	86.3	1129	12	BM924224	BM924224 AGENCOURT
C	19	16.4	86.3	1201	9	AL553402	AL553402 AL553402
C	20	16.4	86.3	1201	13	EX439049	EX439049 EX439049
C	21	16.4	86.3	1987	10	AW888223	AW888223 MXRA8 Hum
C	22	16.4	86.3	435	9	AI329817	AI329817 bf06ne.r
C	23	16.4	84.2	511	9	AI397616	AI397616 NCSC5C8T7
C	24	16.4	84.2	517	9	AW186852	AW186852 BNLGH1597
C	25	16.4	84.2	639	9	AV849197	AV849197 AV849197
C	26	16.4	84.2	648	9	AI398536	AI398536 NCW07A9T7
C	27	16.4	84.2	686	9	AV849138	AV849138 AV849138
C	28	16.4	84.2	701	28	BH954585	BH954585 cdi78612.
C	29	16.4	84.2	709	28	BH954543	BH954543 cdi78612.
C	30	16.4	84.2	831	28	BH423226	BH423226 BOHSZ48TR
C	31	15.8	83.2	192	29	BZ672389	BZ672389 PUBEN32TD
C	32	15.8	83.2	215	9	AV025145	AV025145 AV025145
C	33	15.8	83.2	243	12	BM106925	BM106925 511009 MA
C	34	15.8	83.2	289	13	BQ640964	BQ640964 SSH-Bbb1c
C	35	15.8	83.2	300	9	AU231776	AU231776 AU231776
C	36	15.8	83.2	300	9	AU231871	AU231871 AU231871
C	37	15.8	83.2	300	9	AV181313	AV181313 AV181313
C	38	15.8	83.2	300	14	C55494	C55494 C55494 Yuji
C	39	15.8	83.2	300	14	C57763	C57763 C57763 Yuji
C	40	15.8	83.2	320	28	BZ138443	BZ138443 CH230-256
C	41	15.8	83.2	324	28	BZ137662	BZ137662 CH230-256
C	42	15.8	83.2	347	14	CB225018	CB225018 10M28A01
C	43	15.8	83.2	350	9	AU233974	AU233974 AU233974
C	44	15.8	83.2	353	9	AU278375	AU278375 AU278375
C	45	15.8	83.2	390	28	BH77025	BH77025 fzm5013f0

ALIGNMENTS

RESULT 1  
W92952/c  
LOCUS  
DEFINITION  
W92952 337 bp mRNA linear EST 25-NOV-1996  
IMAGE:356970 5' similar to contains element MER22 repetitive element ;, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
W92952.1 GI:1422104  
Homo sapiens (human)

REFERENCE  
AUTHORS  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P., and Wilson, R.

TITLE  
JOURNAL  
COMMENT  
The WashU-Merck EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estwatson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 998 Std Error: 0.00  
Seq primer: mob.REGA+ET

High quality sequence stop: 279.

## FEATURES

source

Location/Qualifiers

1. .337

/organism="Homo sapiens"

/mol\_type="mrna"

/db\_xref="GDB:1273514"

/db\_xref="taxon:9606"

/clone="IMAGE:356970"

/sex="unknown"

/dev\_stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares fetal heart NbHL19W"

/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site1: Not I; Site2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACATCTGAGTGGAGCGCGCATCTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."

BASE COUNT 63 a 94 c 111 g 67 t 2 others

## ORIGIN

Query Match 86.3%; Score 16.4; DB 14; Length 337;

Best Local Similarity 94.4%; Pred. No. 6.1e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGGG 19

|||||

Db 273 AATGTCATCGTCCCGAG 256

## RESULT 2

AA037563/C

LOCUS

DEFINITION zk34a03.r1 Soares\_pregnant\_uterus\_NbHPU Homo sapiens cDNA clone

IMAGE:484684 5', mRNA sequence.

AA037563

ACCESSION AA037563.1 GI:1512663

VERSION

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Lennon, G., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)

97044478

889549

COMMENT

Contact: Willson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 597 Std Error: 0.00

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 121.

## FEATURES

source

Location/Qualifiers

1. .340

/organism="Homo sapiens"

/mol\_type="mrna"

/db\_xref="GDB:3758398"

/db\_xref="taxon:9606"

/clone="IMAGE:484684"

/sex="female"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="Soares\_pregnant\_uterus\_NbHPU"

/note="Organ: uterus; Vector: pT7T3-Pac; Site1: Not I; Site2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAAGAAATCGCGCCCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."

BASE COUNT 54 a 109 c 115 g 53 t 9 others

## ORIGIN

Query Match 86.3%; Score 16.4; DB 9; Length 340;

Best Local Similarity 94.4%; Pred. No. 6.1e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGGG 19

|||||

Db 35 AATGTCATCGTCCCGAG 18

## RESULT 3

W45082

LOCUS

DEFINITION zk21g10.r1 Soares\_senescent\_fibroblasts\_NbHSP Homo sapiens cDNA

clone IMAGE:323010 5', mRNA sequence.

W45082

ACCESSION W45082.1 GI:1329213

VERSION

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R. The WashU-Merck EST Project Unpublished

TITLE

JOURNAL

COMMENT

Contact: Willson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1423 Std Error: 0.00

Seq primer: mob.REGA+ET

High quality sequence stop: 326.

## FEATURES

source

Location/Qualifiers

1. .369

/organism="Homo sapiens"

/mol\_type="mrna"

/db\_xref="GDB:1254522"

/db\_xref="taxon:9606"

/clone="IMAGE:323010"

/tissue\_type="Senescent fibroblast"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares\_senescent\_fibroblasts\_NbHSP"

/note="Vector: pT7T3D (Pharmacia) with a modified



**W16559**  
**LOCUS** zbl1b12.r1 Soares\_fetal\_lung\_NbHL19W Homo sapiens cDNA clone  
**DEFINITION** IMAGE:301727 5' similar to contains element MSRI repetitive element  
 ; mRNA sequence.  
**ACCESSION** W16559  
**VERSION** W16559.1 GI:1290941  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**REFERENCE** 1 (bases 1 to 537)  
**AUTHORS** Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
**TITLE** The WashU-Merck EST Project  
**JOURNAL** Unpublished  
**COMMENT** Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
**FEATURES** Seq primer: ETPRimer  
 High quality sequence stop: 342.  
 Location/Qualifiers  
 1..537  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:1246658"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:301727"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: lung; Vector: pT73D (Pharmacia) with a modified polylinker; Site\_1: Not 1; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer 15'-TGTACCAATCGAGTGGAGGCGCCGCAATTTTTTTTTTTT-3', double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHL19W."  
**BASE COUNT** 115 a 137 c 164 g 112 t 9 others  
**ORIGIN**  
 Query Match 86.3%; Score 16.4; DB 14; Length 537;  
 Best Local Similarity 94.4%; Pred. No. 7.1e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 AATGTCATCGTCCCGGG 19  
 |||||  
 Db 438 AAAGTCATCGTCCCGGG 455  
 |||||  
**RESULT 8**  
**LOCUS** BI627185 554 bp mRNA linear EST 07-SEP-2001  
**DEFINITION** RH86421.5 prime RH Drosophila melanogaster normalized Head pFlc-1  
 Drosophila melanogaster cDNA clone RH86421.5 similar to lgl:  
 FBan0018285 GO:[ligand binding or carrier (GO:0005488); calmodulin  
 binding (GO:0005516)] located on: 2R 51E5-51E7; 08/24/2001, mRNA  
 sequence.  
**ACCESSION** BI627185  
**VERSION** BI627185.1 GI:15522710  
**KEYWORDS** EST.  
**SOURCE** Drosophila melanogaster (fruit fly)  
**ORGANISM** Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
**REFERENCE** 1 (bases 1 to 554)  
**AUTHORS** Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C. J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Celnikier, S. and Rubin, G. M.  
**TITLE** BDGP/HMI RH Drosophila EST Project  
**JOURNAL** Unpublished  
**COMMENT** Contact: Stapleton, M.  
 BDGP  
 Lawrence Berkeley National Lab  
 One Cyclotron Rd, Berkeley, CA 94720, USA  
 Fax: 510 486 6798

**W16559**  
**LOCUS** 537 bp mRNA linear EST 29-APR-1996  
**DEFINITION** zbl1b12.r1 Soares\_fetal\_lung\_NbHL19W Homo sapiens cDNA clone  
 IMAGE:301727 5' similar to contains element MSRI repetitive element  
 ; mRNA sequence.  
**ACCESSION** W16559  
**VERSION** W16559.1 GI:1290941  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**REFERENCE** 1 (bases 1 to 537)  
**AUTHORS** Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
**TITLE** The WashU-Merck EST Project  
**JOURNAL** Unpublished  
**COMMENT** Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
**FEATURES** Seq primer: ETPRimer  
 High quality sequence stop: 342.  
 Location/Qualifiers  
 1..537  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:1246658"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:301727"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: lung; Vector: pT73D (Pharmacia) with a modified polylinker; Site\_1: Not 1; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer 15'-TGTACCAATCGAGTGGAGGCGCCGCAATTTTTTTTTTTT-3', double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHL19W."  
**BASE COUNT** 115 a 137 c 164 g 112 t 9 others  
**ORIGIN**  
 Query Match 86.3%; Score 16.4; DB 14; Length 537;  
 Best Local Similarity 94.4%; Pred. No. 7.1e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 AATGTCATCGTCCCGGG 19  
 |||||  
 Db 18 AATGTCATCGTCCCGAG 35  
 |||||  
**RESULT 7**  
**LOCUS** AI772402 539 bp mRNA linear EST 18-MAY-2001  
**DEFINITION** EST253502 tomato resistant, Cornell Lycopersicon esculentum cDNA  
 clone cLER2H9, mRNA sequence.  
**ACCESSION** AI772402  
**VERSION** AI772402.1 GI:5270443  
**KEYWORDS** EST.  
**SOURCE** Lycopersicon esculentum (tomato)  
**ORGANISM** Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.  
**REFERENCE** 1 (bases 1 to 539)  
**AUTHORS** D'Ascenzo, M., He, X., Lyman, J., Matern, A. L., Vision, T., Holt, J. E.,  
 Liang, F., Upton, J., Roeding, C. M., Craven, M. B., Fujii, C. Y., Bowman,  
 C. L., Nierman, W., Fraser, C. M., Venter, J. C., Tanksley, S. D.,  
 Giovannoni, J. J. and Martin, G. B.  
**TITLE** Generation of ESTs from Pseudomonas resistant tomato  
**JOURNAL** Unpublished  
**COMMENT** Contact: CUGI  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 5 prime sequence.  
**FEATURES** Location/Qualifiers  
 1..539  
 /organism="Lycopersicon esculentum"  
 /mol\_type="mRNA"  
 /cultivar="R11-12 (35S::Pto in Rio Grande x Money Maker)"  
 /db\_xref="taxon:4081"  
 /clone="CLER2H9"  
 /tissue\_type="leaf"  
 /dev\_stage="4-week old"  
 /lab\_host="SOLR"  
 /clone\_lib="tomato resistant, Cornell"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; cLER - Tomato Pseudomonas Resistant EST Library.  
 Directionally cloned cDNAs inserted into pBluescript SK(-  
 ) at 5' end with EcoRI and 3' end with XhoI site."  
**BASE COUNT** 158 a 118 c 127 g 135 t 1 others  
**ORIGIN**  
 Query Match 86.3%; Score 16.4; DB 9; Length 539;  
 Best Local Similarity 94.4%; Pred. No. 7.1e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 AATGTCATCGTCCCGGG 19  
 |||||  
 Db 438 AAAGTCATCGTCCCGGG 455  
 |||||  
**RESULT 8**  
**LOCUS** BI627185/c 554 bp mRNA linear EST 07-SEP-2001  
**DEFINITION** RH86421.5 prime RH Drosophila melanogaster normalized Head pFlc-1  
 Drosophila melanogaster cDNA clone RH86421.5 similar to lgl:  
 FBan0018285 GO:[ligand binding or carrier (GO:0005488); calmodulin  
 binding (GO:0005516)] located on: 2R 51E5-51E7; 08/24/2001, mRNA  
 sequence.  
**ACCESSION** BI627185  
**VERSION** BI627185.1 GI:15522710  
**KEYWORDS** EST.  
**SOURCE** Drosophila melanogaster (fruit fly)  
**ORGANISM** Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
**REFERENCE** 1 (bases 1 to 554)  
**AUTHORS** Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C. J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Celnikier, S. and Rubin, G. M.  
**TITLE** BDGP/HMI RH Drosophila EST Project  
**JOURNAL** Unpublished  
**COMMENT** Contact: Stapleton, M.  
 BDGP  
 Lawrence Berkeley National Lab  
 One Cyclotron Rd, Berkeley, CA 94720, USA  
 Fax: 510 486 6798



Email: <http://www.fruitfly.org/EST>, [est@fruitfly.berkeley.edu](mailto:est@fruitfly.berkeley.edu)

Plate: RH.684 row: B column: 9

High quality sequence stop: 462.

## FEATURES

source

1. .554  
Location/Qualifiers  
/organism="Drosophila melanogaster"  
/mol\_type="mRNA"  
/db\_xref="taxon:7227"  
/clone="RH68421"  
/sex="male and female"  
/dev\_stage="Adult"  
/lab\_host="DH5-alpha Tona"  
/clone\_lib="FH Drosophila melanogaster normalized head  
pFlc-1"  
/note="Organ: head; Vector: pFlc1; Site:1; XhoI; Site:2;  
BamHI; Library was kindly generated by Piero Carninci at  
the RIKEN. The library was normalized and excised using  
Cre recombinase. Plasmid cDNA library."  
BASE COUNT 177 a 136 c 142 g 99 t  
ORIGIN

Query Match 86.3%; Score 16.4; DB 12; Length 554;  
Best Local Similarity 94.4%; Pred. No. 7.2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 AATGTCATCGTCCCGGG 19  
|||||  
Db 473 AATGTCATCGTCCCGGG 456

RESULT 9  
AW963853  
LOCUS AW963853 562 bp mRNA linear EST 01-JUN-2000  
DEFINITION EST375926 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.  
ACCESSION AW963853  
VERSION AW963853.1 GI:81533689  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 562)  
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt  
I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and  
Quackenbush,J.  
TITLE Assessment of gene expression patterns in a model of colon tumor  
metastasis using a 19,200 element cDNA microarray  
JOURNAL Unpublished  
COMMENT Contact: John Quackenbush  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 3528  
Fax: 301 838 0208  
Email: [johnq@tigr.org](mailto:johnq@tigr.org)  
Plate: 194  
Seq primer: Reverse.

## FEATURES

source

1. .562  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="MAGE resequences, MAGE"  
/note="vector: pBluescriptSKM"  
BASE COUNT 114 a 180 c 159 g 109 t  
ORIGIN

Query Match 86.3%; Score 16.4; DB 10; Length 562;  
Best Local Similarity 94.4%; Pred. No. 7.2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 AATGTCATCGTCCCGGG 19  
|||||  
Db 45 AATGTCATCGTCCCGGG 62

## RESULT 10

BF342569

LOCUS

DEFINITION

BF342569

ACCESSION

BF342569

VERSION

BF342569.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 595)

AUTHORS

NIH-MGC <http://mgc.ncl.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: David N. Louis, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM9411 row: j column: 24

High quality sequence stop: 589.

## FEATURES

source

1. 595  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4149623"  
/tissue\_type="glioblastoma with EGFR amplification"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NCI-CGAP\_Brn64"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site:1: NotI;  
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.57 kb. Constructed by Life  
Technologies. Note: this is a NCI-CGAP Library."  
BASE COUNT 82 a 226 c 195 g 92 t  
ORIGIN

Query Match 86.3%; Score 16.4; DB 10; Length 595;  
Best Local Similarity 94.4%; Pred. No. 7.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGGG 19

|||||

Db 487 AATGTCATCGTCCCGGG 504

## RESULT 11

AL680804/c

LOCUS

DEFINITION

AL680804

ACCESSION

AL680804

VERSION

AL680804.1

KEYWORDS

EST.

SOURCE

Silurana tropicalis (western clawed frog)

ORGANISM

Silurana tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

Xenopodinae; Silurana.

REFERENCE 1 (bases 1 to 623)

AUTHORS

Taylor,R., Ashurst,J.I., Croning,M.D.R., Zorn,A.M. and Rogers,J.

TITLE

Sanger Xenopus tropicalis EST project 2002

JOURNAL

Unpublished

COMMENT

Contact: Taylor R

Sanger Centre

Hinxton, Cambridgeshire, CB10 1SA, UK

Email: tropesanger.ac.uk

Sanger Xenopus tropicalis EST project 2001

TROPICALIS\_SEQUENCE\_ID: Tgas070b10.plcsp6

Sequencing primer: PICSP6

This sequence is from a Xenopus Gene Collection (XGC) library

constructed by Aaron M. Zorn.

#### FEATURES

source

1..623

/organism="Silurana tropicalis"

/mol\_type="mRNA"

/db\_xref="taxon:8364"

/clone="Tgas070b10"

/dev\_stage="gastrula (stages 10.5-13 mixed)"

/lab\_host="Escherichia coli XL1-blue"

/clone\_lib="XGC-gastrula"

/note="Vector: pCS107; Site\_1: EcoRI; Site\_2: NotI; cDNA

was oligo dt primed from 5ug of poly A+ RNA from stages

10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated

into pCS107 with EcoRI at the 5' end and NotI at the 3'

end."

184 a 133 c 153 g 153 t

BASE COUNT  
ORIGIN

Query Match 86.3%; Score 16.4; DB 9; Length 623;

Best Local Similarity 94.4%; Pred. No. 7.5e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCGGG 19

|||||

23 AATGTCATCGTCCCGGG 6

RESULT 12

LOCUS

DEFINITION BGI127540 682 bp mRNA linear EST 31-JAN-2001

EST473282 tomato shoot/meristem Lycopersicon esculentum cDNA clone

CTOF1717 5' sequence, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Lycopersicon esculentum (tomato)

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 682)

AUTHORS

van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,

Hansen,C., Ronning,C. and Tanksley,S.

Generation of ESTs from tomato shoot/meristem tissue

Unpublished

CONTACT: CUGI

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>.

#### FEATURES

source

1..682

/organism="Lycopersicon esculentum"

/mol\_type="mRNA"

/cultivar="TA496"

/db\_xref="taxon:4081"

/clone="CTOF1717"

/tissue\_type="shoot/meristem"

/dev\_stage="developing shoots from 4-6wks old plants"

/lab\_host="SOIR"

/clone\_lib="tomato shoot/meristem"

/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:

XhoI; Small expanding leaves from the growing tip were

taken from greenhouse plants (4-6wks old TA496). Tissue

was immediately frozen in liquid nitrogen."

225 a 135 c 149 g 173 t

BASE COUNT  
ORIGIN

Query Match 86.3%; Score 16.4; DB 10; Length 682;

Best Local Similarity 94.4%; Pred. No. 7.7e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCGGG 19

|||||

405 AATGTCATCGTCCCGGG 422

RESULT 13

LOCUS

DEFINITION BGI758715 768 bp mRNA linear EST 25-SEP-2001

603024016f1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5194610 5',

mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 768)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

CONTACT: Robert Strausberg, Ph.D.

Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLML1486 row: p column: 03

High quality sequence start: 31

High quality sequence stop: 752.

#### FEATURES

source

1..768

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5194610"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_114"

/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;

Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6

male brains, age range 23-27 yo. Library is oligo-dT

primed and directionally cloned (EcoRV site is destroyed

upon cloning). Average insert size 1.5 kb, insert size

range 1-3 Kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 019. Note:

this is a NIH\_MGC Library."

142 a 258 c 243 g 125 t

BASE COUNT  
ORIGIN

Query Match 86.3%; Score 16.4; DB 12; Length 768;

Best Local Similarity 94.4%; Pred. No. 8.1e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCGGG 19

|||||

136 AATGTCATCGTCCCGAG 153

RESULT 14

LOCUS

DEFINITION BGI754114 799 bp mRNA linear EST 25-SEP-2001

603027673f1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5197746 5',

mRNA sequence.

ACCESSION

BGI754114

# VERSION KEYWORDS SOURCE ORGANISM

BI754114.1 GI:15745692  
EST.  
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

# REFERENCE AUTHORS TITLE JOURNAL COMMENT

NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
Plate: L14M11495 row: b column: 19  
High quality sequence stop: 757.

# FEATURES

Location/Qualifiers  
1..799  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5197746"  
/lab\_host="DH103"  
/clone\_lib="NIH\_MGC\_114"

/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6  
male brains, age range 23-27 yo. Library is oligo-dT  
primed and directionally cloned (EcoRV site is destroyed  
upon cloning). Average insert size 1.5 kb, insert size  
range 1-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruher  
(Invitrogen). Research Genetics tracking code 019. Note:  
this is a NIH\_MGC Library."

BASE COUNT 135 a 281 c 261 g 122 t  
ORIGIN

Query Match 86.3%; Score 16.4; DB 12; Length 799;

Best Local Similarity 94.4%; Pred. No. 8.2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGGG 19

Db 368 AATGTCATCGTCCCGAG 385

# RESULT 15 BQ881886 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

BQ881886 903 bp mRNA linear EST 16-AUG-2002  
AGENCOURT\_8726413 NIH\_MGC\_47 Homo sapiens cDNA clone IMAGE:6340913  
5', mRNA sequence.

BQ881886  
BQ881886.1 GI:22273894

EST.

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 903)

NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L14M2538 row: b column: 18

High quality sequence stop: 699.

# FEATURES

source

1..903

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6340913"

/tissue\_type="neuroblastoma, cell line"

/lab\_host="DH103 (phage-resistant)"

/clone\_lib="NIH\_MGC\_47"

/note="Organ: brain; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (life technologies).  
Note: this is a NIH\_MGC Library."

BASE COUNT 160 a 328 c 258 g 155 t

ORIGIN

Query Match 86.3%; Score 16.4; DB 13; Length 903;

Best Local Similarity 94.4%; Pred. No. 8.5e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGGG 19

Db 265 AATGTCATCGTCCCGAG 282

Search completed: August 20, 2003, 04:39:51

Job time : 47.2142 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 01:46:25 ; Search time 1.53722 Seconds  
(without alignments)  
5455.496 Million cell updates/sec

Title: US-09-979-558A-2  
Perfect score: 19  
Sequence: 1 taatgtcatgtcccgagg 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.4	86.3	2132	4	US-09-552-322-1
2	15.4	81.1	2338	4	US-09-582-337-1
3	15.4	81.1	2350	4	US-09-187-478-1
4	15.4	81.1	2350	4	US-09-292-036-1
5	14.8	77.9	99	1	US-08-427-097-12
6	14.8	77.9	99	2	US-08-878-957-12
7	14.8	77.9	170	1	US-08-419-078-5
8	14.8	77.9	170	1	US-08-419-078-6
9	14.8	77.9	170	1	US-08-726-883-5
10	14.8	77.9	170	1	US-08-726-883-6
11	14.8	77.9	300	1	US-08-419-078-4
12	14.8	77.9	300	1	US-08-726-883-4
13	14.8	77.9	384	4	US-09-389-681-451
14	14.8	77.9	384	4	US-09-620-405B-451
15	14.8	77.9	384	4	US-09-433-826B-451
16	14.8	77.9	384	4	US-09-604-287A-451
17	14.8	77.9	1322	1	US-08-419-078-1
18	14.8	77.9	1322	1	US-08-726-883-1
19	14.8	77.9	1752	1	US-08-427-097-13
20	14.8	77.9	1752	1	US-08-427-097-19
21	14.8	77.9	1752	2	US-08-878-957-13
22	14.8	77.9	1752	2	US-08-878-957-19
23	14.4	75.8	601	4	US-09-691-861A-16
24	14.4	75.8	601	4	US-09-691-861A-17
25	14.4	75.8	870	4	US-09-328-352-1475
26	14.4	75.8	1329	1	US-08-278-630A-8
27	14.4	75.8	1356	2	US-08-484-126-4

C	28	14.4	75.8	1356	4	US-09-374-909-4	Sequence 4, Appli
	29	14.4	75.8	2734	4	US-09-143-571-30	Sequence 30, Appli
	30	14.4	75.8	3182	1	US-08-188-582-12	Sequence 12, Appli
	31	14.4	75.8	3182	1	US-08-646-715-12	Sequence 12, Appli
	32	14.4	75.8	9862	4	US-09-691-861A-3	Sequence 3, Appli
	33	14.4	75.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	34	14.2	74.7	881	4	US-09-370-838-288	Sequence 288, App
	35	14.2	74.7	1506	1	US-08-149-105-4	Sequence 4, Appli
	36	14.2	74.7	1506	1	US-08-317-847-4	Sequence 4, Appli
	37	14.2	74.7	1621	2	US-08-933-750C-96	Sequence 96, Appli
	38	14.2	74.7	1621	2	US-09-234-613-96	Sequence 96, Appli
	39	14.2	74.7	1794	3	US-08-123-934A-9	Sequence 9, Appli
	40	14.2	74.7	1794	5	PCT-US94-10080-9	Sequence 9, Appli
	41	14.2	74.7	8224	2	US-09-010-398-14	Sequence 14, Appli
	42	14.2	74.7	8224	3	US-09-366-260-14	Sequence 14, Appli
	43	14.2	74.7	1664976	4	US-08-916-421B-1	Sequence 1, Appli
	44	14	73.7	3888	3	US-08-675-566-12	Sequence 12, Appli
	45	13.8	72.6	645	4	US-09-252-991A-2155	Sequence 2155, Ap

ALIGNMENTS

RESULT 1  
US-09-552-322-1  
; Sequence 1, Application US/09552322  
; Patent No. 6436642  
; GENERAL INFORMATION:  
; APPLICANT: Gould-Rothberg  
; APPLICANT: Rastelli  
; TITLE OF INVENTION: METHOD OF CLASSIFYING A THYROID CARCINOMA USING  
; TITLE OF INVENTION: DIFFERENTIAL GENE EXPRESSION  
; FILE REFERENCE: 15966-548  
; CURRENT APPLICATION NUMBER: US/09/552.322  
; CURRENT FILING DATE: 2000-04-19  
; PRIOR APPLICATION NUMBER: 60/130,123  
; PRIOR FILING DATE: 1999-04-20  
; PRIOR APPLICATION NUMBER: 60/193,203  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 2132  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-552-322-1

Query Match 86.3%; Score 16.4; DB 4; Length 2132;  
Best Local Similarity 94.4%; Pred. No. 25;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATGTCCTCCGGG 19  
DB 844 AATGTCATGTCCTCCGGG 861

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US-09-582-337-1/c  
; Sequence 1, Application US/09582337  
; Patent No. 6562618  
; GENERAL INFORMATION:  
; APPLICANT: Japan Tobacco, Inc.  
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor  
; TITLE OF INVENTION: and Medicinal Uses Thereof  
; FILE REFERENCE: JI-009PCT  
; CURRENT APPLICATION NUMBER: US/09/582.337  
; CURRENT FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: JP P1997-367699  
; PRIOR FILING DATE: 1997-12-25  
; PRIOR APPLICATION NUMBER: JP P1998-356183  
; PRIOR FILING DATE: 1998-12-15  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 1
; LENGTH: 2338
; TYPE: DNA
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(212)
; NAME/KEY: CDS
; LOCATION: (213)..(1256)
; NAME/KEY: 3'UTR
; LOCATION: (1257)..(2338)
; NAME/KEY: polyA_signal
; LOCATION: (2297)..(2302)
; US-09-582-337-1

Query Match      81.1%; Score 15.4; DB 4; Length 2338;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1210 ATGTCATTGTCGCCGGG 1194

RESULT 3
US-09-187-478-1/c
; Sequence 1, Application US/09187478
; Patent No. 6348329
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Brian F.
; TITLE OF INVENTION: Connective Tissue Growth (CTGF) And Methods Of Use
; FILE REFERENCE: 08766/004001
; CURRENT APPLICATION NUMBER: US/09/187,478
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2350
; TYPE: DNA
; ORGANISM: No. 6348329mal Rate Kidney Fibroblast
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (212)..(1252)
US-09-187-478-1

Query Match      81.1%; Score 15.4; DB 4; Length 2350;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ATGTCATCGTCCCGGG 19
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Db      1209 ATGTCATTGTCGCCGGG 1193

RESULT 4
US-09-292-036-1/c
; Sequence 1, Application US/09292036
; Patent No. 6358741
; GENERAL INFORMATION:
; APPLICANT: FIBROGEN, INC
; APPLICANT: SCHMIDT, Brian
; APPLICANT: ALLEN, Margaret
; APPLICANT: SVERDRUP, Fran
; APPLICANT: CARMICHAEL, David
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE
; FILE REFERENCE: FIB100-1
; CURRENT APPLICATION NUMBER: US/09/292,036
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/292,036
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/187,478
; PRIOR FILING DATE: 1998-11-06

; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2350
; TYPE: DNA
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (212)..(1252)
US-09-292-036-1

Query Match      81.1%; Score 15.4; DB 4; Length 2350;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1209 ATGTCATTGTCGCCGGG 1193

RESULT 5
US-08-427-097-12
; Sequence 12, Application US/08427097
; Patent No. 5668294
; GENERAL INFORMATION:
; APPLICANT: Meagher, Richard B.
; APPLICANT: Sommers, Anne O.
; TITLE OF INVENTION: Metal Resistance Sequences and
; TITLE OF INVENTION: Transgenic Plants
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/427,097
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 40-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-427-097-12

Query Match      77.9%; Score 14.8; DB 1; Length 99;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TAATGTCATCGTCCCGG 18
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Db      79 TATTGTCATCGACCCCGG 96
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RESULT 6  
US-08-878-957-12  
; Sequence 12, Application US/08878957  
; Patent No. 5965796  
; GENERAL INFORMATION:  
; APPLICANT: Meagher, Richard B.  
; APPLICANT: Summers, Anne O.  
; APPLICANT: Rugh, Clayton L.  
; TITLE OF INVENTION: Metal Resistance Sequences and  
; TITLE OF INVENTION: Transgenic Plants  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: Colorado  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/878,957  
; FILING DATE: 19-JUN-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/427,097  
; FILING DATE: 21-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferber, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER: 40-94A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 99 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "oligonucleotide"  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-878-957-12  
Query Match 77.9%; Score 14.8; DB 2; Length 99;  
Best Local Similarity 88.9%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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DB 79 TATTGTCATCGACCCCGG 96  
RESULT 7  
US-08-419-078-5/c  
; Sequence 5, Application US/08419078  
; Patent No. 5587306  
; GENERAL INFORMATION:  
; APPLICANT: HAWKINS, PHILLIP R.  
; APPLICANT: SEILHAMER, JEFFREY J.  
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3330 HILLVIEW AVENUE  
; CITY: PALO ALTO

STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/419,078  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PF0030 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-855-0572  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 170 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: Corneal Stroma  
CLONE: 046611  
US-08-419-078-5  
Query Match 77.9%; Score 14.8; DB 1; Length 170;  
Best Local Similarity 88.9%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 AATGTCATCGTCCCGGG 19  
DB 134 AATGTCATCGTCCCGGG 117  
RESULT 8  
US-08-419-078-6/c  
; Sequence 6, Application US/08419078  
; Patent No. 5587306  
; GENERAL INFORMATION:  
; APPLICANT: HAWKINS, PHILLIP R.  
; APPLICANT: SEILHAMER, JEFFREY J.  
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3330 HILLVIEW AVENUE  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/419,078  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PF0030 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-855-0572  
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 170 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE: Fibroblast  
CLONE: 054216  
US-08-419-078-6

Query Match 77.9%; Score 14.8; DB 1; Length 170;  
Best Local Similarity 88.9%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGG 19  
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Db 134 AATGTCATCGTCCCGG 117

RESULT 9  
US-08-726-883-5/c  
Sequence 5, Application US/08726883  
Patent No. 5676946  
GENERAL INFORMATION:  
APPLICANT: HAWKINS, PHILLIP R.  
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3330 HILLVIEW AVENUE  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,883  
FILING DATE: 04-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/419,078  
FILING DATE: 10-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PF0030 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-855-0572  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 170 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE: Fibroblast  
LIBRARY: 054216  
US-08-726-883-5

Query Match 77.9%; Score 14.8; DB 1; Length 170;  
Best Local Similarity 88.9%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGG 19  
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Db 134 AATGTCATCGTCCCGG 117

RESULT 10  
US-08-726-883-6/c  
Sequence 6, Application US/08726883  
Patent No. 5676946  
GENERAL INFORMATION:  
APPLICANT: HAWKINS, PHILLIP R.  
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3330 HILLVIEW AVENUE  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,883  
FILING DATE: 04-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/419,078  
FILING DATE: 10-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PF0030 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-855-0572  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 170 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE: Fibroblast  
LIBRARY: 054216  
US-08-726-883-6

Query Match 77.9%; Score 14.8; DB 1; Length 170;  
Best Local Similarity 88.9%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGG 19  
|||||

Db 134 AATGTCATCGTCCCGG 117

RESULT 11  
US-08-419-078-4/c  
Sequence 4, Application US/08419078  
Patent No. 5587306  
GENERAL INFORMATION:  
APPLICANT: HAWKINS, PHILLIP R.  
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3330 HILLVIEW AVENUE  
CITY: PALO ALTO  
STATE: CA

Db 134 AATGTCATCGTCCCGG 117

RESULT 10  
US-08-726-883-6/c  
Sequence 6, Application US/08726883  
Patent No. 5676946  
GENERAL INFORMATION:  
APPLICANT: HAWKINS, PHILLIP R.  
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3330 HILLVIEW AVENUE  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,883  
FILING DATE: 04-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/419,078  
FILING DATE: 10-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PF0030 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-855-0572  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 170 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE: Fibroblast  
LIBRARY: 054216  
US-08-726-883-6

Query Match 77.9%; Score 14.8; DB 1; Length 170;  
Best Local Similarity 88.9%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGG 19  
|||||

Db 134 AATGTCATCGTCCCGG 117

RESULT 11  
US-08-419-078-4/c  
Sequence 4, Application US/08419078  
Patent No. 5587306  
GENERAL INFORMATION:  
APPLICANT: HAWKINS, PHILLIP R.  
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3330 HILLVIEW AVENUE  
CITY: PALO ALTO  
STATE: CA



COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/419,078  
APPLICATION NUMBER: US/08/419,078  
FILING DATE: 04-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
FILING DATE: 10-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PF0030 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-855-0572  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:  
LIBRARY: Hybrid T/B Lymphoblast  
CLONE: 043866  
US-08-419-078-4

Query Match 77.9%; Score 14.8; DB 1; Length 300;  
Best Local Similarity 88.9%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCGGG 19  
||||| ||| |||||  
Db 256 AATGTCATCTCCACGG 239

RESULT 12  
US-08-726-883-4/c  
; Sequence 4, Application US/08726883  
; Patent No. 5676946  
; GENERAL INFORMATION:  
; APPLICANT: HAWKINS, PHILLIP R.  
; APPLICANT: SELHAMER, JEFFREY J.  
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: INCITE PHARMACEUTICALS, INC.  
; STREET: 3330 HILLVIEW AVENUE  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/726,883  
; FILING DATE: 04-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/419,078  
; FILING DATE: 10-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LUTHER, BARBARA J.  
; REGISTRATION NUMBER: 33954  
; REFERENCE/DOCKET NUMBER: PF0030 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555

TELEFAX: 415-855-0572  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:  
LIBRARY: Hybrid T/B Lymphoblast  
CLONE: 043866  
US-08-726-883-4

Query Match 77.9%; Score 14.8; DB 1; Length 300;  
Best Local Similarity 88.9%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCGGG 19  
||||| ||| |||||  
Db 256 AATGTCATCTCCACGG 239

RESULT 13  
US-09-389-681-451  
; Sequence 451, Application US/09389681A  
; Patent No. 6518237  
; GENERAL INFORMATION:  
; APPLICANT: YUQUI, JIANG  
; APPLICANT: DILLON, DAVIN C.  
; APPLICANT: MITCHAM, JENNIFER L.  
; APPLICANT: XU, JIANGCHUN  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.470C8  
; CURRENT APPLICATION NUMBER: US/09/389,681A  
; CURRENT FILING DATE: 1999-09-02  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 451  
; LENGTH: 384  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(384)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-389-681-451

Query Match 77.9%; Score 14.8; DB 4; Length 384;  
Best Local Similarity 88.9%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCGGG 19  
||||| ||| |||||  
Db 171 AATGTCATCTCCACGG 188

RESULT 14  
US-09-620-405B-451  
; Sequence 451, Application US/09620405B  
; Patent No. 6528054  
; GENERAL INFORMATION:  
; APPLICANT: JIANG, YUQUI  
; APPLICANT: DILLON, DAVIN C.  
; APPLICANT: MITCHAM, JENNIFER L.  
; APPLICANT: XU, JIANGCHUN  
; APPLICANT: HARLOCKER, SUSAN L.  
; APPLICANT: HEPLER, WILLIAM T.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.470C8  
; CURRENT APPLICATION NUMBER: US/09/620,405B  
; CURRENT FILING DATE: 2000-07-20

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; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 451
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(384)
; OTHER INFORMATION: n = A,T,C or G
US-09-620-405B-451

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Query Match      77.9%; Score 14.8; DB 4; Length 384;
Best Local Similarity 88.9%; Pred. NO. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      2 AATGTCATCGTCCCGGG 19
        ||||| ||||| |||||
DB      171 AATGTCATCTCCACGGG 188

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RESULT 15
US-09-433-826B-451
; Sequence 451, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433.826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 451
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(384)
; OTHER INFORMATION: n = A,T,C or G
US-09-433-826B-451

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Query Match      77.9%; Score 14.8; DB 4; Length 384;
Best Local Similarity 88.9%; Pred. NO. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      2 AATGTCATCGTCCCGGG 19
        ||||| ||||| |||||
DB      171 AATGTCATCTCCACGGG 188

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Job time : 5.53722 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 03:41:01 ; Search time 18.9385 Seconds  
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Title: US-09-979-558A-2

Perfect score: 19

Sequence: 1 taatgtcatgtcccgagg 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1517243 seqs, 1124081882 residues

Total number of hits satisfying chosen parameters: 3034486

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA:\*

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	16.4	86.3	1382 14	US-10-102-806-301 Sequence 301, App
2	16.4	86.3	1326 9	US-09-764-853-238 Sequence 238, App
3	16.4	86.3	1387 9	US-09-818-143-20 Sequence 20, Appl
4	16.4	86.3	1389 11	US-09-946-374-76 Sequence 76, Appl
5	16.4	86.3	1389 12	US-10-015-387A-76 Sequence 76, Appl
6	16.4	86.3	1389 12	US-10-006-130A-76 Sequence 76, Appl
7	16.4	86.3	1389 12	US-10-006-172A-76 Sequence 76, Appl
8	16.4	86.3	1389 14	US-10-006-856A-76 Sequence 76, Appl
9	16.4	86.3	1389 14	US-10-006-818A-76 Sequence 76, Appl
10	16.4	86.3	1389 14	US-10-015-393A-76 Sequence 76, Appl
11	16.4	86.3	1389 14	US-10-015-869A-76 Sequence 76, Appl
12	16.4	86.3	1389 14	US-10-012-121A-76 Sequence 76, Appl
13	16.4	86.3	1389 14	US-10-006-116A-76 Sequence 76, Appl
14	16.4	86.3	1389 14	US-10-006-117A-76 Sequence 76, Appl
15	16.4	86.3	1389 14	US-10-017-527A-76 Sequence 76, Appl
16	16.4	86.3	1389 14	US-10-013-913A-76 Sequence 76, Appl

17	16.4	86.3	1389 14	US-10-007-194A-76 Sequence 76, Appl
18	16.4	86.3	1389 14	US-10-013-430A-76 Sequence 76, Appl
19	16.4	86.3	1389 14	US-10-011-671A-76 Sequence 76, Appl
20	16.4	86.3	1389 14	US-10-012-755A-76 Sequence 76, Appl
21	16.4	86.3	1389 14	US-10-015-386A-76 Sequence 76, Appl
22	16.4	86.3	1389 14	US-10-011-692A-76 Sequence 76, Appl
23	16.4	86.3	1389 14	US-10-006-768A-76 Sequence 76, Appl
24	16.4	86.3	1389 14	US-10-017-610A-76 Sequence 76, Appl
25	16.4	86.3	1389 14	US-10-006-063A-76 Sequence 76, Appl
26	16.4	86.3	1389 14	US-10-020-063A-76 Sequence 76, Appl
27	16.4	86.3	1389 14	US-10-015-391A-76 Sequence 76, Appl
28	16.4	86.3	1389 14	US-10-017-407A-76 Sequence 76, Appl
29	16.4	86.3	1389 15	US-10-006-041A-76 Sequence 76, Appl
30	16.4	86.3	1389 15	US-10-011-833A-76 Sequence 76, Appl
31	16.4	86.3	1389 15	US-10-013-822A-76 Sequence 76, Appl
32	16.4	86.3	2040 14	US-10-198-846-10830 Sequence 10830, A
33	16.4	86.3	2132 14	US-10-137-473-1 Sequence 1, Appl
34	16.4	86.3	3152 14	US-10-091-438-274 Sequence 274, App
35	15.8	83.2	268 10	US-09-960-352-14693 Sequence 14693, A
36	15.8	83.2	286 10	US-09-960-352-2142 Sequence 2142, Ap
37	15.8	83.2	286 10	US-09-960-352-3787 Sequence 3787, Ap
38	15.8	83.2	286 10	US-09-960-352-9010 Sequence 9010, Ap
39	15.8	83.2	286 10	US-09-960-352-10176 Sequence 10176, A
40	15.8	83.2	286 10	US-09-960-352-11136 Sequence 11126, A
41	15.8	83.2	286 10	US-09-960-352-13502 Sequence 13502, A
42	15.8	83.2	286 10	US-09-960-352-13526 Sequence 13526, A
43	15.8	83.2	287 10	US-09-960-352-1636 Sequence 1636, Ap
44	15.8	83.2	288 10	US-09-960-352-11141 Sequence 11141, A
45	15.8	83.2	290 10	US-09-960-352-10635 Sequence 10635, A

## ALIGNMENTS

## RESULT 1

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US-10-102-806-301
; Sequence 301, Application US/10102806
; Publication No. US2003005442A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAL03PIC1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 301
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (22)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (223)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1840)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1849)
; OTHER INFORMATION: n equals a,t,g, or c
; OTHER INFORMATION: n equals a,t,g, or c
US-10-102-806-301
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Query Match 86.3%; Score 16.4; DB 14; Length 1882;  
Best Local Similarity 94.4%; Pred. No. 53;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGGG 19  
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 Db 529 AATGTCATCGTCCCGAG 546

## RESULT 2

US-09-764-853-238  
 ; Sequence 238, Application US/09764853  
 ; Patent No. US20020090672A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PJ206  
 ; CURRENT APPLICATION NUMBER: US/09/764,853  
 ; CURRENT FILING DATE: 2001-01-17  
 ; Prior application data removed - consult PALM or file wrapper  
 ; NUMBER OF SEQ ID NOS: 939  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 238  
 ; LENGTH: 1926  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-764-853-238

Query Match 86.3%; Score 16.4; DB 9; Length 1926;

Best Local Similarity 94.4%; Pred. No. 53;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGGG 19  
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 Db 573 AATGTCATCGTCCCGAG 590

## RESULT 3

US-09-818-143-20  
 ; Sequence 20, Application US/09818143  
 ; Patent No. US20020019000A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walker, Michael G.  
 ; APPLICANT: Voikmuth, Wayne  
 ; APPLICANT: Klingler, Tod M.  
 ; TITLE OF INVENTION: POLYNUCLEOTIDES COEXPRESSED WITH MATRIX-REMODELING GENES  
 ; FILE REFERENCE: PB-0004 CIP  
 ; CURRENT APPLICATION NUMBER: US/09/818,143  
 ; CURRENT FILING DATE: 2001-03-26  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 20  
 ; LENGTH: 1987  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: 3948614CB1  
 US-09-818-143-20

Query Match 86.3%; Score 16.4; DB 9; Length 1987;

Best Local Similarity 94.4%; Pred. No. 53;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGGG 19  
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 Db 716 AATGTCATCGTCCCGAG 733

## RESULT 4

US-09-946-374-76  
 ; Sequence 76, Application US/09946374  
 ; Publication No. US20030073129A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2830PIC1  
 ; CURRENT APPLICATION NUMBER: US/09/946,374  
 ; CURRENT FILING DATE: 2001-09-04  
 ; PRIOR APPLICATION NUMBER: 60/098716  
 ; PRIOR FILING DATE: 1998-09-01  
 ; PRIOR APPLICATION NUMBER: 60/098723  
 ; PRIOR FILING DATE: 1998-09-01  
 ; PRIOR APPLICATION NUMBER: 60/098749  
 ; PRIOR FILING DATE: 1998-09-01  
 ; PRIOR APPLICATION NUMBER: 60/098750  
 ; PRIOR FILING DATE: 1998-09-01  
 ; PRIOR APPLICATION NUMBER: 60/098803  
 ; PRIOR FILING DATE: 1998-09-02  
 ; PRIOR APPLICATION NUMBER: 60/098821  
 ; PRIOR FILING DATE: 1998-09-02  
 ; PRIOR APPLICATION NUMBER: 60/098843  
 ; PRIOR FILING DATE: 1998-09-02  
 ; PRIOR APPLICATION NUMBER: 60/099536  
 ; PRIOR FILING DATE: 1998-09-09  
 ; PRIOR APPLICATION NUMBER: 60/099596  
 ; PRIOR FILING DATE: 1998-09-09  
 ; PRIOR APPLICATION NUMBER: 60/099598  
 ; PRIOR FILING DATE: 1998-09-09  
 ; PRIOR APPLICATION NUMBER: 60/099602  
 ; PRIOR FILING DATE: 1998-09-09  
 ; PRIOR APPLICATION NUMBER: 60/099642  
 ; PRIOR FILING DATE: 1998-09-09  
 ; PRIOR APPLICATION NUMBER: 60/099741  
 ; PRIOR FILING DATE: 1998-09-10  
 ; PRIOR APPLICATION NUMBER: 60/099754  
 ; PRIOR FILING DATE: 1998-09-10  
 ; PRIOR APPLICATION NUMBER: 60/099763  
 ; PRIOR FILING DATE: 1998-09-10  
 ; PRIOR APPLICATION NUMBER: 60/099792  
 ; PRIOR FILING DATE: 1998-09-10  
 ; PRIOR APPLICATION NUMBER: 60/099808  
 ; PRIOR FILING DATE: 1998-09-10  
 ; PRIOR APPLICATION NUMBER: 60/099812  
 ; PRIOR FILING DATE: 1998-09-10  
 ; PRIOR APPLICATION NUMBER: 60/099815  
 ; PRIOR FILING DATE: 1998-09-10  
 ; PRIOR APPLICATION NUMBER: 60/099816  
 ; PRIOR FILING DATE: 1998-09-10  
 ; PRIOR APPLICATION NUMBER: 60/100385  
 ; PRIOR FILING DATE: 1998-09-15  
 ; PRIOR APPLICATION NUMBER: 60/100388  
 ; PRIOR FILING DATE: 1998-09-15  
 ; PRIOR APPLICATION NUMBER: 60/100390  
 ; PRIOR FILING DATE: 1998-09-15  
 ; PRIOR APPLICATION NUMBER: 60/100584  
 ; PRIOR FILING DATE: 1998-09-16  
 ; PRIOR APPLICATION NUMBER: 60/100627



; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2830P1654  
 ; CURRENT APPLICATION NUMBER: US/10/015,387A  
 ; CURRENT FILING DATE: 2001-12-12  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 477  
 ; SEQ ID NO 76  
 ; LENGTH: 1989  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-015-387A-76

Query Match 86.3%; Score 16.4; DB 12; Length 1989;  
 Best Local Similarity 94.4%; Pred. No. 53;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 AATGTCATCGTCCCGGG 19  
 |||||  
 Db 715 AATGTCATCGTCCCGAG 732

RESULT 6  
 US-10-006-130A-76  
 ; Sequence 76, Application US/10006130A  
 ; Publication No. US20030148375A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan I.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2830P167  
 ; CURRENT APPLICATION NUMBER: US/10/006,130A  
 ; CURRENT FILING DATE: 2002-03-19  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 477  
 ; SEQ ID NO 76  
 ; LENGTH: 1989  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-006-130A-76

Query Match 86.3%; Score 16.4; DB 12; Length 1989;  
 Best Local Similarity 94.4%; Pred. No. 53;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 AATGTCATCGTCCCGGG 19  
 |||||  
 Db 715 AATGTCATCGTCCCGAG 732

RESULT 7  
 US-10-006-172A-76  
 ; Sequence 76, Application US/10006172A  
 ; Publication No. US2003015300A1  
 ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan I.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2830P1611  
 ; CURRENT APPLICATION NUMBER: US/10/006,172A  
 ; CURRENT FILING DATE: 2002-03-19  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 477  
 ; SEQ ID NO 76  
 ; LENGTH: 1989  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-006-172A-76

Query Match 86.3%; Score 16.4; DB 12; Length 1989;  
 Best Local Similarity 94.4%; Pred. No. 53;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 AATGTCATCGTCCCGGG 19  
 |||||  
 Db 715 AATGTCATCGTCCCGAG 732

;; PRIOR APPLICATION NUMBER: 60/100664  
;; PRIOR FILING DATE: 1998-09-16  
;; PRIOR APPLICATION NUMBER: 60/100683  
;; PRIOR FILING DATE: 1998-09-17  
;; PRIOR APPLICATION NUMBER: 60/100684  
;; PRIOR FILING DATE: 1998-09-17  
;; PRIOR APPLICATION NUMBER: 60/100710  
;; PRIOR FILING DATE: 1998-09-17  
;; PRIOR APPLICATION NUMBER: 60/100711  
;; PRIOR FILING DATE: 1998-09-17  
;; PRIOR APPLICATION NUMBER: 60/100848  
;; PRIOR FILING DATE: 1998-09-18  
;; PRIOR APPLICATION NUMBER: 60/100849  
;; PRIOR FILING DATE: 1998-09-18  
;; PRIOR APPLICATION NUMBER: 60/100919  
;; PRIOR FILING DATE: 1998-09-17  
;; PRIOR APPLICATION NUMBER: 60/100930  
;; PRIOR FILING DATE: 1998-09-17  
;; PRIOR APPLICATION NUMBER: 60/101014  
;; PRIOR FILING DATE: 1998-09-18  
;; PRIOR APPLICATION NUMBER: 60/101068  
;; PRIOR FILING DATE: 1998-09-18  
;; PRIOR APPLICATION NUMBER: 60/101071  
;; PRIOR FILING DATE: 1998-09-18  
;; PRIOR APPLICATION NUMBER: 60/101279  
;; PRIOR FILING DATE: 1998-09-22  
;; PRIOR APPLICATION NUMBER: 60/101471  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101472  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101474  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101475  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101476  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101477  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101479  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101738  
;; PRIOR FILING DATE: 1998-09-24  
;; PRIOR APPLICATION NUMBER: 60/101741  
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;; PRIOR APPLICATION NUMBER: 60/101743  
;; PRIOR FILING DATE: 1998-09-24  
;; PRIOR APPLICATION NUMBER: 60/101915  
;; PRIOR FILING DATE: 1998-09-24  
;; PRIOR APPLICATION NUMBER: 60/101916  
;; PRIOR FILING DATE: 1998-09-24  
;; PRIOR APPLICATION NUMBER: 60/102207  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102240  
;; PRIOR FILING DATE: 1998-09-29  
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;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102330  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102331  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102484  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102487  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102570  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102571  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102684  
;; PRIOR FILING DATE: 1998-10-01  
;; PRIOR APPLICATION NUMBER: 60/102687  
;; PRIOR FILING DATE: 1998-10-01  
;; PRIOR APPLICATION NUMBER: 60/102965

;; PRIOR FILING DATE: 1998-10-02  
;; PRIOR APPLICATION NUMBER: 60/103258  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103314  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103315  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103328  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103395  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103396  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103401  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103449  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103633  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103678  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103679  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103711  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/104257  
;; PRIOR FILING DATE: 1998-10-14  
;; PRIOR APPLICATION NUMBER: 60/104987  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105000  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105002  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105104  
;; PRIOR FILING DATE: 1998-10-21  
;; PRIOR APPLICATION NUMBER: 60/105169  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105266  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105693  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105694  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105807  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/105881  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/105882  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/106023  
;; PRIOR FILING DATE: 1998-10-28

Query Match 86.3%; Score 16.4; DB 12; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 53;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATGTCCTCCCGGG 19  
|||||  
DB 715 AATGTCATGTCCTCCCGAG 732

RESULT 8  
US-10-006-856A-76  
; Sequence 76, Application US/10006856A  
; Publication No. US2003004941A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang



```

; Publication No. US20030069179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Praonl, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: Acids Encoding the Same
; FILE REFERENCE: P2830PIC45
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-869A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AATGTCATCGTCCCGGG 19
        ||||||
DB       715 AATGTCATCGTCCCGAG 732

RESULT 11
US-10-015-869A-76
; Sequence 76, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Praonl, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: Acids Encoding the Same
; FILE REFERENCE: P2830PIC45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-869A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      2 AATGTCATCGTCCCGGG 19
Db      715 AATGTCATCGTCCCGAG 732

RESULT 12
US-10-012-121A-76
; Sequence 76, Application US/10012121A
; Publication No. US20030073810A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Piont, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C20
; CURRENT APPLICATION NUMBER: US/10/012.121A
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-121A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AATGTCATCGTCCCGGG 19
Db      715 AATGTCATCGTCCCGAG 732

RESULT 13
US-10-006-116A-76
; Sequence 76, Application US/10006116A
; Publication No. US20030082626A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Piont, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C15
; CURRENT APPLICATION NUMBER: US/10/006.116A
; CURRENT FILING DATE: 2001-12-16
; Prior Application Number: 60/098716
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098723
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098749
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098750
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098803
; Prior Filing Date: 1998-09-02
; Prior Application Number: 60/098821
; Prior Filing Date: 1998-09-02
; Prior Application Number: 60/098843
; Prior Filing Date: 1998-09-02
; Prior Application Number: 60/099536
; Prior Filing Date: 1998-09-09
; Prior Application Number: 60/099596
; Prior Filing Date: 1998-09-09
; Prior Application Number: 60/099598
; Prior Filing Date: 1998-09-09
; Prior Application Number: 60/099602
; Prior Filing Date: 1998-09-09
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; Prior Application Number: 60/099741
; Prior Filing Date: 1998-09-10
; Prior Application Number: 60/099754
; Prior Filing Date: 1998-09-10
; Prior Application Number: 60/099763
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; Prior Filing Date: 1998-09-10
; Prior Application Number: 60/099816
; Prior Filing Date: 1998-09-10
; Prior Application Number: 60/100385
; Prior Filing Date: 1998-09-15
; Prior Application Number: 60/100388
; Prior Filing Date: 1998-09-15
; Prior Application Number: 60/100390
; Prior Filing Date: 1998-09-15
; Prior Application Number: 60/100584
; Prior Filing Date: 1998-09-16
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; Prior Filing Date: 1998-09-17
; Prior Application Number: 60/100684
; Prior Filing Date: 1998-09-17
; Prior Application Number: 60/100710
; Prior Filing Date: 1998-09-17
; Prior Application Number: 60/100711
; Prior Filing Date: 1998-09-17
; Prior Application Number: 60/100848
; Prior Filing Date: 1998-09-18
; Prior Application Number: 60/100849
; Prior Filing Date: 1998-09-18
; Prior Application Number: 60/100919
; Prior Filing Date: 1998-09-17
; Prior Application Number: 60/100930
; Prior Filing Date: 1998-09-17
; Prior Application Number: 60/101014
; Prior Filing Date: 1998-09-18
; Prior Application Number: 60/101068
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;; PRIOR FILING DATE: 1998-09-18  
;; PRIOR APPLICATION NUMBER: 60/101071  
;; PRIOR FILING DATE: 1998-09-18  
;; PRIOR APPLICATION NUMBER: 60/101279  
;; PRIOR FILING DATE: 1998-09-22  
;; PRIOR APPLICATION NUMBER: 60/101471  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101472  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101474  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101475  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101476  
;; PRIOR FILING DATE: 1998-09-23  
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;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101479  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101738  
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;; PRIOR FILING DATE: 1998-10-01  
;; PRIOR APPLICATION NUMBER: 60/102965  
;; PRIOR FILING DATE: 1998-10-02  
;; PRIOR APPLICATION NUMBER: 60/103258  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103314  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103315  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103328  
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;; PRIOR APPLICATION NUMBER: 60/103395  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103396  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103401  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103449  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103633  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103678  
;; PRIOR FILING DATE: 1998-10-08

;; PRIOR APPLICATION NUMBER: 60/103679  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103711  
;; PRIOR FILING DATE: 1998-10-08  
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;; PRIOR APPLICATION NUMBER: 60/104987  
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;; PRIOR APPLICATION NUMBER: 60/105000  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105002  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105104  
;; PRIOR FILING DATE: 1998-10-21  
;; PRIOR APPLICATION NUMBER: 60/105169  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105266  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105693  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105694  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105807  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/105881  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/105882  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/106023  
;; PRIOR FILING DATE: 1998-10-28

Query Match 86.3%; Score 16.4; DB 14; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 53;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGGG 19  
|||||  
DB 715 AATGTCATCGTCCCGAG 732

## RESULT 14

US-10-006-117A-76  
; Sequence 76, Application US/10006117A  
; Publication NO. US20030082627A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C13  
; CURRENT APPLICATION NUMBER: US/10/006,117A  
; CURRENT FILING DATE: 2002-03-19  
; Prior Application removed.- See File Wrapper or Palm  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 477  
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US-10-006-117A-76

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoli, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P28301C63
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; CURRENT FILING DATE: 2001-12-13
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; PRIOR APPLICATION NUMBER: 60/098723
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Search completed: August 20, 2003, 06:42:14
Job time : 19.9385 secs

Query Match 86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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